

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 8, 2005, 09:49:12 ; Search time 9268.38 Seconds
(without alignments)
11250.684 Million cell updates/sec

Title: US-09-841-894A-16

Perfect score: 2152
Sequence: 1 GGGGCTGTACCAAGGCGGCGTC.....AAGCTTCTTATATGTTTA 2152

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenBank:

1: gb_ba: *
2: gb_hg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_srs: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2152	100.0	2152	6	AR112295 Sequence
2	2150	99.9	3306	6	BC050416 Homo sapi
3	2088	97.0	2904	6	AR278710 Sequence
4	2088	97.0	2904	6	AR400442 Sequence
5	2088	97.0	2904	6	AR405709 Sequence
6	2088	97.0	2904	6	AR564089 Sequence
7	2088	97.0	2904	6	AX200994 Sequence
8	2088	97.0	2904	6	AX267729 Sequence
9	2029	94.3	3320	6	AX327336 Sequence
10	1972	91.6	2143	6	AR112294 Sequence
11	1968	91.4	4034	6	AR400443 Sequence
12	1968	91.4	4034	6	AR400443 Sequence
13	1968	91.4	4034	6	AR405710 Sequence
14	1968	91.4	4034	6	AR564089 Sequence
15	1968	91.4	4034	6	AX200995 Sequence
16	1968	91.4	4034	6	AX267730 Sequence
17	1936	90.0	4894	6	AR278709 Sequence
18	1936	90.0	4894	6	AR400441 Sequence
19	1936	90.0	4894	6	AR405708 Sequence

20	1936	90.0	4894	6	AR564088 Sequence
21	1936	90.0	4894	6	AX200993 Sequence
22	1936	90.0	4894	6	AX267728 Sequence
23	1919	89.2	3410	6	BD242022 Compounds
24	1919	89.2	3410	6	AR237205 Sequence
25	1919	89.2	3410	6	AR278229 Sequence
26	1919	89.2	3410	6	AR366925 Sequence
27	1919	89.2	3410	6	AR370821 Sequence
28	1919	89.2	3410	6	AR392326 Sequence
29	1919	89.2	3410	6	AR399961 Sequence
30	1919	89.2	3410	6	AR405228 Sequence
31	1919	89.2	3410	6	AR439432 Sequence
32	1919	89.2	3410	6	AR563608 Sequence
33	1919	89.2	3410	6	AX106329 Sequence
34	1919	89.2	3410	6	AX140620 Sequence
35	1919	89.2	3410	6	AX200480 Sequence
36	1919	89.2	3410	6	AX267136 Sequence
37	1919	89.2	3410	6	AX429961 Sequence
38	1919	89.2	3410	6	BD070258 Compounds
39	1919	89.2	3410	9	AY033593 Homo sapi
40	1823	84.7	6976	6	AR278712 Sequence
41	1823	84.7	6976	6	AR400444 Sequence
42	1823	84.7	6976	6	AR405711 Sequence
43	1823	84.7	6976	6	AR564091 Sequence
44	1823	84.7	6976	6	AX200996 Sequence
45	1823	84.7	6976	6	AX267731 Sequence

ALIGNMENTS

RESULT 1
AR112295
LOCUS AR112295 Sequence 16 from patent US 6130043.
DEFINITION AR112295
ACCESSION AR112295
VERSION AR112295.1 GI:14092195
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2152)
AUTHORS Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Roberts-Rapp, L., Russell, J.C., Stroupe, S.D. and Yu, H.
TITLE Regents and methods useful for detecting diseases of the prostate
JOURNAL Patent: US 6130043-A 16 10-OCT-2000;
FEATURES
source 1. 2152
/organism="unknown"
/mol_type="unasigned DNA"

ORIGIN

Query Match 100.0%; Score 2152; DB 6; Length 2152;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGCTGTACCAAGGCGGCGTCGAGCTGAGCCGCGGACCGAGGCGGAGACATATGA 60
1 GGGGCTGTACCAAGGCGGCGTCGAGCTGAGCCGCGGACCGAGGCGGAGACATATGA 60
DB 1 GGGGCTGTACCAAGGCGGCGTCGAGCTGAGCCGCGGACCGAGGCGGAGACATATGA 60
QY 61 TGAAGCGCTTCGATGGGCAAGCTGGGCGCTGTTCTGTCAGTGGCCATCTCCCTGGTCTT 120
61 TGAAGCGCTTCGATGGGCAAGCTGGGCGCTGTTCTGTCAGTGGCCATCTCCCTGGTCTT 120
DB 61 TGAAGCGCTTCGATGGGCAAGCTGGGCGCTGTTCTGTCAGTGGCCATCTCCCTGGTCTT 120
QY 121 CTCTCTGTCATGAGACCGGCTGGTGCAGGATTCGGCACTCGAGCAAGTATTTGGCCAG 180
121 CTCTCTGTCATGAGACCGGCTGGTGCAGGATTCGGCACTCGAGCAAGTATTTGGCCAG 180
DB 121 CTCTCTGTCATGAGACCGGCTGGTGCAGGATTCGGCACTCGAGCAAGTATTTGGCCAG 180
QY 181 TGTGGCAGCTTCCCTGTGGCTGCGGTCGCCATGCTGTGCCACAGTGTGGCCGTGGT 240
181 TGTGGCAGCTTCCCTGTGGCTGCGGTCGCCATGCTGTGCCACAGTGTGGCCGTGGT 240
DB 181 TGTGGCAGCTTCCCTGTGGCTGCGGTCGCCATGCTGTGCCACAGTGTGGCCGTGGT 240

QY	241	GACACCTTCAAGCCGCGCCCTCAACCGGGTTACCTTCTCAAGCCTCTGAGATCTCTGCCCTAAC	300
Db	241	GACAGCTTCAGCCGCCCTCTCAACCGGGTTACCTTCTCAAGCCTCTGAGATCTCTGCCCTAAC	300
QY	301	ACTGGCCTCCCTCTACACACCGGAGGAAGCAGGTGTTCTGTGCCAAATACGAGGGGACAC	360
Db	301	ACTGGCCTCCCTCTACACACCGGAGGAAGCAGGTGTTCTGTGCCAAATACGAGGGGACAC	360
QY	361	TGGAGGTCTAGCAGTGAAGGACACCTTGATGACCAAGCTTCTGTCCAGGECCTTAAGCTGG	420
Db	361	TGGAGGTCTAGCAGTGAAGGACACCTTGATGACCAAGCTTCTGTCCAGGECCTTAAGCTGG	420
QY	421	AGCTCCCTTCCCTAATGAGCAACGTGGGTGTGAGAGCAGTGGCCGTGCTCCACTCCAC	480
Db	421	AGCTCCCTTCCCTAATGAGCAACGTGGGTGTGAGAGCAGTGGCCGTGCTCCACTCCAC	480
QY	481	CGGCTCTGCGGGGGCCTTGTGCTGTATGTCTCCGTACGTGTGTGTGGTGAAGCCAC	540
Db	481	CGGCTCTGCGGGGGCCTTGTGCTGTATGTCTCCGTACGTGTGTGTGGTGAAGCCAC	540
QY	541	CGAGGCCAGAGGTGGTTCCGGGCGGGGACATCTGTCTGAGACCTTGCCATCTGTGATGTGC	600
Db	541	CGAGGCCAGAGGTGGTTCCGGGCGGGGACATCTGTCTGAGACCTTGCCATCTGTGATGTGC	600
QY	601	CTTCTCTGTCTCCCAAGGTGGCCCATCTCTGTTTATGTGGCTCCATTGTCCAGCTGACCA	660
Db	601	CTTCTCTGTCTCCCAAGGTGGCCCATCTCTGTTTATGTGGCTCCATTGTCCAGCTGACCA	660
QY	661	GTCGTCTACGCTAATATGGTGTCTGCGGAGGCGGGGTGTGTGTGCGCATTTATCTTTGG	720
Db	661	GTCGTCTACGCTAATATGGTGTCTGCGGAGGCGGGGTGTGTGTGCGCATTTATCTTTGG	720
QY	721	TACACAGTATGATTTTGAACAAGCGACTTGGCCAAATATCAGCGTATGAAAACCTTCCAG	780
Db	721	TACACAGTATGATTTTGAACAAGCGACTTGGCCAAATATCAGCGTATGAAAACCTTCCAG	780
QY	781	CACATTGGGGGTGAGAGGGCCGTGCTCACTGGGGTCCAGCTCCCGCTCTCTGTTAGCCCAT	840
Db	781	CACATTGGGGGTGAGAGGGCCGTGCTCACTGGGGTCCAGCTCCCGCTCTCTGTTAGCCCAT	840
QY	841	GGGGCTGCCGGCTGGCCGCCAGTTTCTGTGCTGTCGCAAAATATGTGGCTCTGTGCTGC	900
Db	841	GGGGCTGCCGGCTGGCCGCCAGTTTCTGTGCTGTCGCAAAATATGTGGCTCTGTGCTGC	900
QY	901	CACCTGTGCTCTAGAGTGGGTACTGCTCAACGCTGGGGGCTGGGCGCTCCCTCTCTCT	960
Db	901	CACCTGTGCTCTAGAGTGGGTACTGCTCAACGCTGGGGGCTGGGCGCTCCCTCTCTCTCT	960
QY	961	CTTCCCAAGTCTCTAGGGCTGTGCTGTGACTGGAGGCTTCCAAAGGGGTTTCAAGTCTGAACTT	1020
Db	961	CTTCCCAAGTCTCTAGGGCTGTGCTGTGACTGGAGGCTTCCAAAGGGGTTTCAAGTCTGAACTT	1020
QY	1021	ATACAGGGAGGCGAAGGGCTCCATGCACTGGAATGCGGGGACTCTGCAAGTGTGATTAAC	1080
Db	1021	ATACAGGGAGGCGAAGGGCTCCATGCACTGGAATGCGGGGACTCTGCAAGTGTGATTAAC	1080
QY	1081	CCAGGCTCAGGGTTAAACGCTAAGCTCTCTAAGTATGAGCAACACTTATGAGAAAGGTTTTTGG	1140
Db	1081	CCAGGCTCAGGGTTAAACGCTAAGCTCTCTAAGTATGAGCAACACTTATGAGAAAGGTTTTTGG	1140
QY	1141	GAGCGAATAAATCACTGACACTGTGTTTCCCATTTCTAAGCCCTTTAACTGTGACGTTG	1200
Db	1141	GAGCGAATAAATCACTGACACTGTGTTTCCCATTTCTAAGCCCTTTAACTGTGACGTTG	1200
QY	1201	TTTATATGATCTTGTGATGGAGATTTCTAGATGAAACACTCTCTCAATGGGATTTTGAAC	1260
Db	1201	TTTATATGATCTTGTGATGGAGATTTCTAGATGAAACACTCTCTCAATGGGATTTTGAAC	1260
QY	1261	ATATGAAAGTTATTTGTAGGGGAAAGTCTGTGAGGGGCAACACAAAGAACCAAGTCCCC	1320
Db	1261	ATATGAAAGTTATTTGTAGGGGAAAGTCTGTGAGGGGCAACACAAAGAACCAAGTCCCC	1320
QY	1321	TCAGCCCAAGCACTGTCTTTTGTGTGATGCACACCCCTTTACCTTTATCAGAGATGTG	1380

Db	1321	TCAGCCCAAGCACTGCTCTTTTGGCTGATCACCCCCTTACCTTTATTCAGGATGTC	138
QY	1381	GCGCTGTGCTCTTCTGTGTCATCAAGAGACAGAGCACTTTAAATATTAACTTAATT	144
Db	1381	GCGCTGTGCTCTTCTGTGTCATCAAGAGACAGAGCACTTTAAATATTAACTTAATT	144
QY	1441	ATTTAACTTAAGTAAAGGAAATCAATGTGTAAGCTTTCTGTGTGTGTCTAATATTTGG	150
Db	1441	ATTTAACTTAAGTAAAGGAAATCAATGTGTAAGCTTTCTGTGTGTGTCTAATATTTGG	150
QY	1501	GTAAGGTGGGGATATCCCAACAATCAAGTCCCTGAGTAAGTGTGTCTATTTGGCTGATCA	156
Db	1501	GTAAGGTGGGGATATCCCAACAATCAAGTCCCTGAGTAAGTGTGTCTATTTGGCTGATCA	156
QY	1561	TTGCCAGAAATCTTCTTCTCTGTGGGTGTGGCCCCCAAAATGCTTAACCCAGACCTTGG	162
Db	1561	TTGCCAGAAATCTTCTTCTCTGTGGGTGTGGCCCCCAAAATGCTTAACCCAGACCTTGG	162
QY	1621	AAATTTACTCAATCCCAAAATGATAATTCCTTCAATGCTGTATCCCAAGTTAAGGTTTGA	168
Db	1621	AAATTTACTCAATCCCAAAATGATAATTCCTTCAATGCTGTATCCCAAGTTAAGGTTTGA	168
QY	1681	GGAAAGTAGAGGTGGGGCTTCAGGCTCAACAGGCTCCCTTAACCAACCCCTTCTCTTGG	174
Db	1681	GGAAAGTAGAGGTGGGGCTTCAGGCTCAACAGGCTCCCTTAACCAACCCCTTCTCTTGG	174
QY	1741	GGCCAGGCTGTGTCCCCCACTTTCACATCCCTCTTACTCTGTAGAAGTGGCTGATGA	180
Db	1741	GGCCAGGCTGTGTCCCCCACTTTCACATCCCTCTTACTCTGTAGAAGTGGCTGATGA	180
QY	1801	AGGCACTGCCAAAATTTCCCTCAACCCCACTTTCCTCCCTAACCCTTCCCACTTCCCACTA	186
Db	1801	AGGCACTGCCAAAATTTCCCTCAACCCCACTTTCCTCCCTAACCCTTCCCACTTCCCACTA	186
QY	1861	GCTCCACAACCTGTGTGAGCTACTGAGGACCAAGACCAAGACCAAGTGCCTTCCCAAG	192
Db	1861	GCTCCACAACCTGTGTGAGCTACTGAGGACCAAGACCAAGACCAAGTGCCTTCCCAAG	192
QY	1921	CCTTGTGTCATCTGAGGCCCCAGATATCTGTGCTTTGGGAATCTTCAACAGAAATCTC	198
Db	1921	CCTTGTGTCATCTGAGGCCCCAGATATCTGTGCTTTGGGAATCTTCAACAGAAATCTC	198
QY	1981	AGAGACAACCCCTGCTGAGCTAAGGAGGCTTATCTCAAGGAGGGGTTTAAGTCCG	204
Db	1981	AGAGACAACCCCTGCTGAGCTAAGGAGGCTTATCTCAAGGAGGGGTTTAAGTCCG	204
QY	2041	TTTGCATTAATGTGCTTATTTATTTTAAAGGGGTGAATTTTATATCTGAAGTGAACA	210
Db	2041	TTTGCATTAATGTGCTTATTTATTTTAAAGGGGTGAATTTTATATCTGAAGTGAACA	210
QY	2101	ATCAGAGTATATGTTATGTGACAAAATTAAGGCTTCTTAATATGTTTA 2152	
Db	2101	ATCAGAGTATATGTTATGTGACAAAATTAAGGCTTCTTAATATGTTTA 2152	

RESULT_2						PRI 30-JUN-2004
LOCUS	BC050416					
DEFINITION	Homo sapiens	3306 bp	mRNA	linear		
	prostatein protein, mRNA (CDNA clone MGC:540920					
	IMAGE:6189823), complete cds.					
ACCESSION	BC050416					
VERSION	BC050416.2	GI:34194585				
KEYWORDS	MGC.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Bukacynska, Metzger; Chiodate; Cranlate; Vertebrate; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
	1 (Dases 1 to 3306)					
	Straussberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,					
	Klausner,R.D., Collins,F.S., Wagner,L., Shennan,C.M., Schuler,G.D.,					
	Altschul,S.F., Zeeberg,B., Buecaw,K.H., Schaefer,C.F., Bhak,N.K.,					
	Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,D., Hsieh,F.,					

Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uedin, T.B., Toshimuki, S., Carinini, P., Prange, C., Rana, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunatane, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.U., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Small, D.B., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 3306)

Struhsberg, R.

Direct Submission

Submitted (08-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>

On Aug. 25, 2003 this sequence version replaced gi:29791944.

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-shgc.stanford.edu>

Contact: (Dickson, Mark) mcddpaxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>

Series: IRAX Plate: 98 Row: n Column: 14

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14916436.

Location/Qualifiers

1. .3306

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="MGC:54090 IMAGE:6198823"

/issue_type="Peripheral Nervous System, sympathetic trunk"

/clone_1fb="Lupski_sympathetic_trunk"

/lab_host="DH10B"

/note="Vector: pCMV-SPORT6"

1.3306

/gene="Protein"

/note="synonym: PRST"

/db_xref="LocustID:85414"

/db_xref="MIM:608319"

248_ .1909

/gene="Protein"

/codon_start=1

/product="protein protein"

/protein_id="AAH50416.1"

/db_xref="GI:29791945"

/db_xref="LocustID:85414"

/db_xref="MIM:608319"

/translation="WQRLVSRLLRHRKAQLLVNLTFFGSEVCLAAGITVPELLLEVGVEKMTWLVGIPVGLVCPPLGSDHMRGVRPRPFWALSGLLSLFLIPRAGMLGLCPDRPLELALLIGVGLGCGVCFPLBALSLDFRDHDSROAYSVAFMISLGGCLGLPAILDMDTSAAPYVGTCGCLFGLTLTILFVCVATLLVAEEAALGPTEBPAGLAPSLSPHCCPRALAFRNIGALLPRHQLCCMRPLRLFLV

ALGSMWLMFTLLPYTDFVGBGLYGVPRAPRGTEARRHYDEGVMSGLFLCAI
SLVRSUNDRIVVORGTAVVLAASVAPVPAAGATCLSHSVAVTASALNPTFSAL
QLPFTLASLHREKQVLPVKRTGTGASDSISLTSPVPPKRAPFNHVGAG
SGLLPPALPCASACDVSVRVVEPPEAPVPRGICLDAIILDSAPLISQVAPSL
FMGISVLOSQSVTAVMVASAAGLVAIVATQVVDKSLAKYSA"

ORIGIN

Query Match	Best Local Similarity	Score	DB	Length	3306;
1	GGGGCTGTACAGAGGCGTGTCCAGAGCTGAGCCGGGACCGGAGACACATATGA	60			
1141	GGGGCTGTACAGAGGCGTGTCCAGAGCTGAGCCGGGACCGGAGACACATATGA	1200			
61	TGAAGGCGTTGGATAGGAGCGCTGGGGCTGTCTCGAGTGCAGTCCCTGTGCTT	120			
1201	TGAAGGCGTTGGATAGGAGCGCTGGGGCTGTCTCGAGTGCAGTCCCTGTGCTT	1260			
121	CTCTCTGTGATGACCGGCTGTGTGACAGATTTGGCACTCGAGCATTTATTTGGCAG	180			
1261	CTCTCTGTGATGACCGGCTGTGTGACAGATTTGGCACTCGAGCATTTATTTGGCAG	1320			
181	TGTGAGAGCTTCCCTGTGTGAGTGTGCGGTGACATGCTGTCCAGAGTGTGGCTGT	240			
1321	TGTGAGAGCTTCCCTGTGTGAGTGTGCGGTGACATGCTGTCCAGAGTGTGGCTGT	1380			
241	GACAGCTTACGCGCGCTTACCGGGTTCACCTTTCAGCGCTGCAGATCTGCTTACAC	300			
1381	GACAGCTTACGCGCGCTTACCGGGTTCACCTTTCAGCGCTGCAGATCTGCTTACAC	1440			
301	ACTGAGCTTCCCTGTGTACACCGGAGAGAGAGTGTTCCTGCGCAATACCGAGGGACAC	360			
1441	ACTGAGCTTCCCTGTGTACACCGGAGAGAGAGTGTTCCTGCGCAATACCGAGGGACAC	1500			
361	TGAGAGGTGTACAGATGAGAGACAGCTGTATGACAGCTTCTGCGAGGCTTAAGCTGTG	420			
1501	TGAGAGGTGTACAGATGAGAGACAGCTGTATGACAGCTTCTGCGAGGCTTAAGCTGTG	1560			
421	AGCTCCCTTCCCTTAATGACAGCTGTGTGTGTGAGGACAGTGTGCTTCCACCTTCACC	480			
1561	AGCTCCCTTCCCTTAATGACAGCTGTGTGTGTGAGGACAGTGTGCTTCCACCTTCACC	1620			
481	CGCGCTTGTGCGGGGCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	540			
1621	CGCGCTTGTGCGGGGCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1680			
541	CGAGGCGAGGGGTGTTCGCGGCGCGGAGCATGTGCGGAGCTCGGCATCTGATGTATGTC	600			
1681	CGAGGCGAGGGGTGTTCGCGGCGCGGAGCATGTGCGGAGCTCGGCATCTGATGTATGTC	1740			
601	CTTCTGTGTGTCCAGAGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	660			
1741	CTTCTGTGTGTCCAGAGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1800			
661	GTCTGTCACTGCTTATATGT	720			
1801	GTCTGTCACTGCTTATATGT	1860			
721	TACACAGGTATATTTGACAGAGGCACTTGTGCAAAATPCTAGCGTAAACATTTCCAG	780			
1861	TACACAGGTATATTTGACAGAGGCACTTGTGCAAAATPCTAGCGTAAACATTTCCAG	1920			
781	CACATTGGGGTGAAGGCGCTGTGCTTCACTGAGTCCAGCTCCCGCTCTGTATAGCCCAT	840			
1921	CACATTGGGGTGAAGGCGCTGTGCTTCACTGAGTCCAGCTCCCGCTCTGTATAGCCCAT	1980			
841	GGGGCTGTGCGGGGCTGGCGGCGAGTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	900			
1981	GGGGCTGTGCGGGGCTGGCGGCGAGTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2040			
901	CACCGTGTGCTGTAGGT	960			

Db	2041	CACCCTGTGCGTGAAGTGTCCGTAAGCTGCACAGCTGTGGGGGCTGGGGGCTCCCTCTCTCT	2100
Qy	961	CTCCCCAGTCTCTAAGGCTGTGCTGACTGAGAGGCTTTCAGAGGGGTTTCAGTCTGAAGCTT	1020
Db	2101	CTCCCCAGTCTCTAAGGGCTGTGCTGACTGAGAGGCTTTCAGAGGGGTTTCAGTCTGAAGCTT	2160
Qy	1021	ATACAGGAGGCGCAGAAAGGGCTCCATAGCACTGGAAATGGGGGACCTCTGCAAGTGGATTAC	1080
Db	2161	ATACAGGAGGCGCAGAAAGGGCTCCATAGCACTGGAAATGGGGGACCTCTGCAAGTGGATTAC	2220
Qy	1081	CCAGGCTCAGGGTTAAACAGCTAGCCCTCTAGTTAGACACACTGAGAAAGGGTTTTTGG	1140
Db	2221	CCAGGCTCAGGGTTAAACAGCTAGCCCTCTAGTTAGACACACTGAGAAAGGGTTTTTGG	2280
Qy	1141	GACSTGAATTAATCTCAGTCAACCTGGTTTCCCAATCTCTAAGCCCTTAACTCTGACGTTGG	1200
Db	2281	GACSTGAATTAATCTCAGTCAACCTGGTTTCCCAATCTCTAAGCCCTTAACTCTGACGTTGG	2340
Qy	1201	TTTAAATGAGCTCTTGCAATGGAGTTTCTAGATGAAACACTCTCCATGGGATTTTGAAC	1260
Db	2341	TTTAAATGAGCTCTTGCAATGGAGTTTCTAGATGAAACACTCTCCATGGGATTTTGAAC	2400
Qy	1261	ATATGAAGTTAATTTGATGGGGAABAAGTCTGAGGGGCAACACACAGAACCAAGTCCCC	1320
Db	2401	ATATGAAGTTAATTTGATGGGGAABAAGTCTGAGGGGCAACACACAGAACCAAGTCCCC	2460
Qy	1321	TCAGCCACAGACACTGTCTTTTGTGTGATACACCCGCTCTTACTCTTTATCAGGATGTG	1380
Db	2461	TCAGCCACAGACACTGTCTTTTGTGTGATACACCCGCTCTTACTCTTTATCAGGATGTG	2520
Qy	1381	GCCTGTGGTCTCTGCTGTGTCATACACAGACACAGGCAATTAATATTTAACTTAATTT	1440
Db	2521	GCCTGTGGTCTCTGCTGTGTCATACACAGACACAGGCAATTAATATTTAACTTAATTT	2580
Qy	1441	ATTTAACAAAGTAGAAGGGAATCCATTGCTAGCTTTTCTGTGTGGTGTCTAATATTTGG	1500
Db	2581	ATTTAACAAAGTAGAAGGGAATCCATTGCTAGCTTTTCTGTGTGGTGTCTAATATTTGG	2640
Qy	1501	GTAAGGTGGGGATATCCCAACATCAGGTCCCTGAGATAGCTGTGATTTGGGCTGATCA	1560
Db	2641	GTAAGGTGGGGATATCCCAACATCAGGTCCCTGAGATAGCTGTGATTTGGGCTGATCA	2700
Qy	1561	TTGCAGATCTTCTTCTCTGGGGGTGTGGGCCCCCAAAATGGCTAACCCAGACCTTGTG	1620
Db	2701	TTGCAGATCTTCTTCTCTGGGGGTGTGGGCCCCCAAAATGGCTAACCCAGACCTTGTG	2760
Qy	1621	AAATTTCTACTATCCCAATATGATTAATTCAAATGCTGTTAACCCAGAGTTAGGTTGTGAA	1680
Db	2761	AAATTTCTACTATCCCAATATGATTAATTCAAATGCTGTTAACCCAGAGTTAGGTTGTGAA	2820
Qy	1681	GAAAGGTAGAGGTGGGGCTTCAAGTGTCAACGGCTTCCCTAACACCCCTCTTCTTGG	1740
Db	2821	GAAAGGTAGAGGTGGGGCTTCAAGTGTCTCAACGGCTTCCCTAACACCCCTCTTCTTGG	2880
Qy	1741	GCCCAAGCTGTGTTCCCCCACTTGCACGTCCCTCTACTCTCTCTAGAGACTGGGCTGATGA	1800
Db	2881	GCCCAAGCTGTGTTCCCCCACTTGCACGTCCCTCTACTCTCTCTAGAGACTGGGCTGATGA	2940
Qy	1801	AGGCACTGCCCCAAATTTTCCCTAACCCCCCAACTTTCCCTCAACCCCAACTTTTCCCAACA	1860
Db	2941	AGGCACTGCCCCAAATTTTCCCTAACCCCCCAACTTTTCCCTCAACCCCAACTTTTCCCAACA	3000
Qy	1861	GCTCCACAACCTGTTTGAAGCTACTGACAGACCAAGAACACAACAAGTGGGTTTCCCAAG	1920
Db	3001	GCTCCACAACCTGTTTGAAGCTACTGACAGACCAAGAACACAACAAGTGGGTTTCCCAAG	3060
Qy	1921	CCTTTGTCCATCTCAGCCCCCAAGATATCTGTGCTTGGGGAATCTCACAGAAATCTC	1980
Db	3061	CCTTTGTCCATCTCAGCCCCCAAGATATCTGTGCTTGGGGAATCTCACAGAAATCTC	3120
Qy	1981	AGGAGCACCCCTGCTGAGACTTAAGGAGAGTCTTAATCTCTCAGAGGGGGGTTTAAGTGGCG	2040
Db	3121	AGGAGCACCCCTGCTGAGACTTAAGGAGAGTCTTAATCTCTCAGAGGGGGGTTTAAGTGGCG	3180

[illegible]

QY 605 CTGCTGCTCCAGAGTGGCCCGCCATCCCTGTTTATGAGGCTCCATGTCAGGCTCAGCCAGTCT 664
 DB 1353 CTGCTGTCCAGAGTGGCCCGCCATCCCTGTTTATGAGGCTCCATGTCAGGCTCAGCCAGTCT 1412
 QY 665 GTCACTGCTTATGATGTCGTGCGGAGGCTGGGCTGTGGTGGCCATTACTTACTTGTCTACA 724
 DB 1413 GTCACTGCTTATGATGTCGTGCGGAGGCTGGGCTGTGGTGGCCATTACTTACTTGTCTACA 1472
 QY 725 CAGGATGATTTTGAACAAGACGACTTGGCCAAATTACTCAGCGTGAAGAACTTCCAGACACA 784
 DB 1473 CAGGATGATTTTGAACAAGACGACTTGGCCAAATTACTCAGCGTGAAGAACTTCCAGACACA 1532
 QY 785 TTGGGGTGAAGAGGCTGCTCACTGGGCTCCAGCTCCCGCTCTCTGTAGCCCAATGGG 844
 DB 1533 TTGGGGTGAAGAGGCTGCTCACTGGGCTCCAGCTCCCGCTCTCTGTAGCCCAATGGG 1592
 QY 845 CTGCGGGCTGGCCGCGCAGTTTCTGTGTCGCAAGTATGATGAGTCTCTGCTGCGCAC 904
 DB 1593 CTGCGGGCTGGCCGCGCAGTTTCTGTGTCGCAAGTATGATGAGTCTCTGCTGCGCAC 1652
 QY 905 CTGTGCTGCTGAGTGCAGTACGACAGCTGGGGGCTGGGGGCTCTCTCTCTCTCTCC 964
 DB 1653 CTGTGCTGCTGAGTGCAGTACGACAGCTGGGGGCTGGGGGCTCTCTCTCTCTCTCC 1712
 QY 965 CCAAGTCTTAGAGGCTGCTGACGTGAGGCTTCAAGGGGCTTCAAGTCTGACCTTATAC 1024
 DB 1713 CCAAGTCTTAGAGGCTGCTGACGTGAGGCTTCAAGGGGCTTCAAGTCTGACCTTATAC 1772
 QY 1025 AGGAGAGCCAGAAAGGCTCATGACATGGAATGCGGGGACTCTGACAGTGGATTACCCAG 1084
 DB 1773 AGGAGAGCCAGAAAGGCTCATGACATGGAATGCGGGGACTCTGACAGTGGATTACCCAG 1832
 QY 1085 GCTCAGAGGTTAACAGCTAGCCTCTAGTTGAGACACACCTAGAGAGGCTTTTGGAGC 1144
 DB 1833 GCTCAGAGGTTAACAGCTAGCCTCTAGTTGAGACACACCTAGAGAGGCTTTTGGAGC 1892
 QY 1145 TGAATTAATCACTGACCTGCTGCTTCCCATCTCTAAGCCCTTAACTGACGCTTCTTAA 1204
 DB 1893 TGAATTAATCACTGACCTGCTGCTTCCCATCTCTAAGCCCTTAACTGACGCTTCTTAA 1952
 QY 1205 ATGAGCTCTTGCATGAGGATTTCTAGATGAAACACTCTCCATGGGATTTGAACATAT 1264
 DB 1953 ATGAGCTCTTGCATGAGGATTTCTAGATGAAACACTCTCCATGGGATTTGAACATAT 2012
 QY 1265 GAAAGTATTTGAGGAGGAGTCTTGAAGGCGCAACAAGAACAGGCTCCCTCAG 1324
 DB 2013 GAAAGTATTTGAGGAGGAGTCTTGAAGGCGCAACAAGAACAGGCTCCCTCAG 2072
 QY 1325 CCCACGACCTGCTTTTGTGCTGATCACCCCTCTTACCTTTATACAGATGGCT 1384
 DB 2073 CCCACGACCTGCTTTTGTGCTGATCACCCCTCTTACCTTTATACAGATGGCT 2132
 QY 1385 GTTGGCTCTTGTGCTGATCACAGAGACAGGCAATTAATTAATTAATTAATTAATTAAT 1444
 DB 2133 GTTGGCTCTTGTGCTGATCACAGAGACAGGCAATTAATTAATTAATTAATTAATTAAT 2192
 QY 1445 AACAAAGTGAAGGAGATCATGCTAGCTTTTCTGTGTGTGTCTAAATTTTGGGTAG 1504
 DB 2193 AACAAAGTGAAGGAGATCATGCTAGCTTTTCTGTGTGTGTCTAAATTTTGGGTAG 2252
 QY 1505 GGTGGGGATTCGCCAACATCAAGTCTCCCTGAGATGCTGTGCTATTTGGGCTGATCTTC 1564
 DB 2253 GGTGGGGATTCGCCAACATCAAGTCTCCCTGAGATGCTGTGCTATTTGGGCTGATCTTC 2312
 QY 1565 CAGAACTCTTCTCTCTGCGGCTGCGCCGCAAAATGCTAAACAGAGACCTTGGAAAT 1624
 DB 2313 CAGAACTCTTCTCTCTGCGGCTGCGCCGCAAAATGCTAAACAGAGACCTTGGAAAT 2372
 QY 1625 TCTACTCATCCCAATGATTAATTCAAATGCTGTTCACCAAGTTAGGGTGTGAAGAA 1684
 DB 2373 TCTACTCATCCCAATGATTAATTCAAATGCTGTTCACCAAGTTAGGGTGTGAAGAA 2432

QY 1685 GGTAGAGGGTGGGGGCTTCAGGTCTCAAGGCTTCCCTAACCAACCCCTCTCTTGGGCC 1744
 DB 2433 GGTAGAGGGTGGGGGCTTCAGGTCTCAAGGCTTCCCTAACCAACCCCTCTCTTGGGCC 2492
 QY 1745 AGCTGCTTCCCGCCCACTTCACTCCCTCTACTCTCTAGAGCTGGCTGATGAAGC 1804
 DB 2493 AGCTGCTTCCCGCCCACTTCACTCCCTCTACTCTCTAGAGCTGGCTGATGAAGC 2552
 QY 1805 ACTGCCAAATTTTCCCTAACCCCAACTTTCCTTACCCCAACTTTCCTTCCAGCTC 1864
 DB 2553 ACTGCCAAATTTTCCCTAACCCCAACTTTCCTTACCCCAACTTTCCTTCCAGCTC 2612
 QY 1865 CACAACCTGTTTGAAGTACTGACAGGACCAAGACCAAGAGTGGCTTCCAGGCTT 1924
 DB 2613 CACAACCTGTTTGAAGTACTGACAGGACCAAGACCAAGAGTGGCTTCCAGGCTT 2672
 QY 1925 TGTCCATCTCAGCCCGCAGAGTATCTGTGCTGGGGAATCTCACAGAAACTCAGGA 1984
 DB 2673 TGTCCATCTCAGCCCGCAGAGTATCTGTGCTGGGGAATCTCACAGAAACTCAGGA 2732
 QY 1985 GCAACCCCTGCTGAGCTAAGGAGGCTTATCTCTCAGGGGGGTTTAACTCCGTTG 2044
 DB 2733 GCAACCCCTGCTGAGCTAAGGAGGCTTATCTCTCAGGGGGGTTTAACTCCGTTG 2792
 QY 2045 CAAATATGCTGCTTATTTATTTAGCGGGGTGAATTTTATATCTGATGACATCA 2104
 DB 2793 CAAATATGCTGCTTATTTATTTAGCGGGGTGAATTTTATATCTGATGACATCA 2852
 QY 2105 GAGTATATGTTTATGATGACAAATTTAAAGCTTCTTATATGTTTA 2152
 DB 2853 GAGTATATGTTTATGATGACAAATTTAAAGCTTCTTATATGTTTA 2900

RESULT 4
 AR400442
 LOCUS AR400442 2904 bp DNA linear PAT 18-DEC-2003
 DEFINITION Sequence 703 from patent US 6620922.
 ACCESSION AR400442
 VERSION AR400442.1 GI:40143818
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 2904)
 Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
 Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
 Vedrick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W.,
 Hepler,W.T. and Henderson,R.A.
 Compositions and methods for the therapy and diagnosis of prostate
 cancer
 Patent: US 6620922-A 703 16-SEP-2003;
 JOURNAL Location/Qualifiers
 FEATURES
 source 1..2904
 /organism="unknown"
 /mol_type="genomic DNA"
 ORIGIN
 Query Match 97.0%; Score 2088; DB 6; Length 2904;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2088; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 GGGCTTGGATGGGACGCTGGGGCTGTTCTGCACTGCGCATCTCCCTGCTTCTCT 124
 DB 813 GGGCTTGGATGGGACGCTGGGGCTGTTCTGCACTGCGCATCTCCCTGCTTCTCT 872
 QY 125 CTGGTATGAGACCGGCTGGTGAAGGATTCGGCACTCGAGCATCTAATTTGGCAGTGTG 184
 DB 873 CTGGTATGAGACCGGCTGGTGAAGGATTCGGCACTCGAGCATCTAATTTGGCAGTGTG 932
 QY 185 GCAGCTTTCCTGTGGCTGCGGCTGCAATGCTGTCCACAGTGTGGCGGTGTGACA 244
 DB 933 GCAGCTTTCCTGTGGCTGCGGCTGCAATGCTGTCCACAGTGTGGCGGTGTGACA 992

QY	245	GCTTCAGCGCGCCCTGACCGGGTTGACCTTTCAGCGCCCTGCAATCTGCGCTTACACACTG	304
Db	993	GCTTCAGCGCGCCCTGACCGGGTTGACCTTTCAGCGCCCTGCAATCTGCGCTTACACACTG	1052
QY	305	GCTTCCTCTACACCGGGAGAGAGAGGTGTTCTGCGCCAAATCCGAGGGGACACTGGA	364
Db	1053	GCTTCCTCTACACCGGGAGAGAGAGGTGTTCTGCGCCAAATCCGAGGGGACACTGGA	1112
QY	365	GGTGTGACAGTGAAGACAGCTGATGACAGCTTCCGCGAGGACCTTAAGCCCTGAAGCT	424
Db	1113	GGTGTGACAGTGAAGACAGCTGATGACAGCTTCCGCGAGGACCTTAAGCCCTGAAGCT	1172
QY	425	CCCTTCCCTAATGAGACAGTGGGTGCTGAGAGCAGTGGCCGCTGACCTCCACCTCCAGCCG	484
Db	1173	CCCTTCCCTAATGAGACAGTGGGTGCTGAGAGCAGTGGCCGCTGACCTCCACCTCCAGCCG	1232
QY	485	CTTCGCGGGGCTCTGCTGTGATGTCTCCGTACGTGTGGTGTGGGTGAGCCACCGAG	544
Db	1233	CTTCGCGGGGCTCTGCTGTGATGTCTCCGTACGTGTGGTGTGGGTGAGCCACCGAG	1292
QY	545	GCCAGGGTGGTTCGCGGCGGGGAGATCGGCTGAGACCTGCGCATCTCTGATGATGCTTC	604
Db	1293	GCCAGGGTGGTTCGCGGCGGGGAGATCGGCTGAGACCTGCGCATCTCTGATGATGCTTC	1352
QY	605	CTGCTGTCCAGAGTGGGCCCATCCGTGTTATGGGCTCCATGTGCCAGCTCAGCCAGTCT	664
Db	1353	CTGCTGTCCAGAGTGGGCCCATCCGTGTTATGGGCTCCATGTGCCAGCTCAGCCAGTCT	1412
QY	665	GTCACATCCCTAATAGGTGTCTGCGCGAGCGCTGGGTCTGTGTGCTGCTTATCTTGTCTA	724
Db	1413	GTCACATCCCTAATAGGTGTCTGCGCGAGCGCTGGGTCTGTGTGCTGCTTATCTTGTCTA	1472
QY	725	CAGGTAGTATTTGACAGAGCGAGCTTGCCAAATATCTAGCGCTGAGAAACTTCACAGACA	784
Db	1473	CAGGTAGTATTTGACAGAGCGAGCTTGCCAAATATCTAGCGCTGAGAAACTTCACAGACA	1532
QY	785	TGCGGGTGAAGGGGCTGCTCCTCAGTGGGTCCAGCTCCGCTCTGTTAGCCCAAGGAG	844
Db	1533	TGCGGGTGAAGGGGCTGCTCCTCAGTGGGTCCAGCTCCGCTCTGTTAGCCCAAGGAG	1592
QY	845	CTGCGCGGGTGGCGCGCAGTTCGTGTGCTGCCAAATGATGGGTCTCTCTGCTGCTCC	904
Db	1593	CTGCGCGGGTGGCGCGCAGTTCGTGTGCTGCCAAATGATGGGTCTCTCTGCTGCTCC	1652
QY	905	CTGTGCTGCTAGGTGCTGAGTCTGACAGACTGGGGCTGGGGGCTCCCTCTCTCTCTCC	964
Db	1653	CTGTGCTGCTAGGTGCTGAGTCTGACAGACTGGGGCTGGGGGCTCCCTCTCTCTCTCC	1712
QY	965	CCAGTCTCTAGGGGCTGCTGACGTGAGAGGCTTCCAAAGGGGTTTCAATCTGACTTATAC	1024
Db	1713	CCAGTCTCTAGGGGCTGCTGACGTGAGAGGCTTCCAAAGGGGTTTCAATCTGACTTATAC	1772
QY	1025	AGGAGAGCCAGAAAGGGCTTCATGCACTGAAATGCGGGGACTCTGCAAGGTGATTAACCGAG	1084
Db	1773	AGGAGAGCCAGAAAGGGCTTCATGCACTGAAATGCGGGGACTCTGCAAGGTGATTAACCGAG	1832
QY	1085	GCTCAGGGTTAACAGTACGCTCCTCTAATGAGACACACTTGAAGAAAGGCTTTTGGAGG	1144
Db	1833	GCTCAGGGTTAACAGTACGCTCCTCTAATGAGACACACTTGAAGAAAGGCTTTTGGAGG	1892
QY	1145	TGAATTAATCTAGTCACTGTTTCCCATCTCTAAGCCCTTAACTGCACTTCTGTTA	1204
Db	1893	TGAATTAATCTAGTCACTGTTTCCCATCTCTAAGCCCTTAACTGCACTTCTGTTA	1952
QY	1205	ATGTAGCTCTTGAAGTGAAGTTCATGAGATGAACACTCTCTCATGGGATTTGAACATAT	1264
Db	1953	ATGTAGCTCTTGAAGTGAAGTTCATGAGATGAACACTCTCTCATGGGATTTGAACATAT	2012
QY	1265	GAAAGTATTTGTAGGGAGAGTCTGAGGGGGAACAACAAGAACAGGTCCCTCAG	1324
Db	2013	GAAAGTATTTGTAGGGAGAGTCTGAGGGGGAACAACAAGAACAGGTCCCTCAG	2072
QY	1325	CCCAAGACACTGTCTTTTGTGTGATCCACCCCTCTTACTTATCAGAGTGTGAGCT	1384

Db	2073	CCCAAGACACTGTCTTTTGTGTGATCCACCCCTCTTACTTATCAGAGTGTGAGCT	2132
QY	1385	GTTGGTCTCTTCTGTTGCCATCAACAGACACAGGATTTAAATTTATTTATTTATTT	1444
Db	2133	GTTGGTCTCTTCTGTTGCCATCAACAGACACAGGATTTAAATTTATTTATTTATTTATTT	2192
QY	1445	AACAAAGTGAAGGGAATCATTTGCTAGCTTTCTGTGTGGTGTCTAATTTTGGGTAG	1504
Db	2193	AACAAAGTGAAGGGAATCATTTGCTAGCTTTCTGTGTGGTGTCTAATTTTGGGTAG	2252
QY	1505	GGTGGGGATCCCAACAATAGTCCCTGAGATGCTGATCATTTGGGCTGATTTGC	1564
Db	2253	GGTGGGGATCCCAACAATAGTCCCTGAGATGCTGATCATTTGGGCTGATTTGC	2312
QY	1565	CAGAACTCTCTCTGCTGGGGCTGGCCCCCAAAATGCTTAACTCCAGACCTTGGAAAT	1624
Db	2313	CAGAACTCTCTCTGCTGGGGCTGGCCCCCAAAATGCTTAACTCCAGACCTTGGAAAT	2372
QY	1625	TCTACTCATCCCAATGATTAATCCAAATGCTGTTACCAAGTGAAGGCTTGAAGGA	1684
Db	2373	TCTACTCATCCCAATGATTAATCCAAATGCTGTTACCAAGTGAAGGCTTGAAGGA	2432
QY	1685	GGTAGAAGGTGGGCTTCAAGTCTCAAGGCTTCCCTAACCACTTCTCTTGGCCC	1744
Db	2433	GGTAGAAGGTGGGCTTCAAGTCTCAAGGCTTCCCTAACCACTTCTCTTGGCCC	2492
QY	1745	AGCTGTTCCTCCCACTTCCACTCCCTCTACTCTCTGATGAGACTGGGCTGATGAAGG	1804
Db	2493	AGCTGTTCCTCCCACTTCCACTCCCTCTACTCTCTGATGAGACTGGGCTGATGAAGG	2552
QY	1805	ACTGCCCCAAATTTCCCTTACCCCAACTTTCCTTACCCCACTTTCCTTCCACAGCTC	1864
Db	2553	ACTGCCCCAAATTTCCCTTACCCCAACTTTCCTTACCCCACTTTCCTTCCACAGCTC	2612
QY	1865	CACAACCTGTTTGAAGTACTGAGAGACAGAGACCAAGAGCAAAAGCGGTTTCCCAAGCTT	1924
Db	2613	CACAACCTGTTTGAAGTACTGAGAGACAGAGACCAAGAGCAAAAGCGGTTTCCCAAGCTT	2672
QY	1925	TGTCATCTCAAGCCCAAGATATCTGTGCTGGGAAATCTCACAGAACTCAGGA	1984
Db	2673	TGTCATCTCAAGCCCAAGATATCTGTGCTGGGAAATCTCACAGAACTCAGGA	2732
QY	1985	GCACCCCTGCTGAGTGAAGGAGTCTTATCTCTCAGGGGGGTTAAAGTCCGTTG	2044
Db	2733	GCACCCCTGCTGAGTGAAGGAGTCTTATCTCTCAGGGGGGTTAAAGTCCGTTG	2792
QY	2045	CAATTAATGCTCTTATTTATTTAGCGGGTGAATATTTATTACTGTAAGTGAATCA	2104
Db	2793	CAATTAATGCTCTTATTTATTTAGCGGGTGAATATTTATTACTGTAAGTGAATCA	2852
QY	2105	GAGTAAATGTTTATGTCACAAATTAAGGCTTCTTATATGTTTA	2152
Db	2853	GAGTAAATGTTTATGTCACAAATTAAGGCTTCTTATATGTTTA	2900

RESULT 5
AR405709
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 2904)
AUTHORS
XU, Y., DILLON, D.C., MITCHAM, J.L., HARLOCKER, S.L., JIANG, Y.,
KALOS, M.D., FANGER, G.R., RETZER, M.W., STOLK, J.A., DAY, C.H.,
VEDVICK, T.S., CARTER, D., LI, S.X., WANG, A., SKEIKY, Y.A.W.,
HEPLER, W.T. and HENDERSON, R.A.
Compositions and methods for the therapy and diagnosis of prostate
cancer

JOURNAL Patent: US 6630305-A 703 07-Oct-2003;
FEATURES Location/Qualifiers
Source 1..2904
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 97.0%; Score 2088; DB 6; Length 2904;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 2088; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 65 GGCCTTCGATGGGACAGCCCTGGGGCTGTTCTCTGACAGTGGCCATCTCCCTGGCTTCTCT 124
DB 813 GGCCTTCGATGGGACAGCCCTGGGGCTGTTCTCTGACAGTGGCCATCTCCCTGGCTTCTCT 872
QY 125 CTGCTCATGAGACCGGCTGGTGCAGCGATTCCGGCACTCGACAGTCTATTGGCCAGTGTG 184
DB 873 CTGCTCATGAGACCGGCTGGTGCAGCGATTCCGGCACTCGACAGTCTATTGGCCAGTGTG 932
QY 185 GCAAGCTTTCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 244
DB 933 GCAAGCTTTCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 992
QY 245 GCTTCAGCCGCTTCACCGGCTTCACTTCTGAGCCCTGAGATCTGCTGCTGCTGCTGCTGCT 304
DB 993 GCTTCAGCCGCTTCACCGGCTTCACTTCTGAGCCCTGAGATCTGCTGCTGCTGCTGCTGCT 1052
QY 305 GCTTCCTCTTACCAACCGGAGAAAGAGGTCTTCTGCGCAATATCCGAGGGGACACTGGA 364
DB 1053 GCTTCCTCTTACCAACCGGAGAAAGAGGTCTTCTGCGCAATATCCGAGGGGACACTGGA 1112
QY 365 GGTGCTAGAGATGAGACAGCTGATGACAGCTTCTGCGAGCCCTTAAGCTTGAAGCT 424
DB 1113 GGTGCTAGAGATGAGACAGCTGATGACAGCTTCTGCGAGCCCTTAAGCTTGAAGCT 1172
QY 425 CCCTTCCCTAATGAGACAGTGGGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 484
DB 1173 CCCTTCCCTAATGAGACAGTGGGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1232
QY 485 CTCTGCGGGGCTCTGCTGCTGATGCTCTCGTACGTGTGAGTGGGTGAGCCACCGAG 544
DB 1233 CTCTGCGGGGCTCTGCTGCTGATGCTCTCGTACGTGTGAGTGGGTGAGCCACCGAG 1292
QY 545 GGCAGGGTGGTCCCGGGCCGGGCACTCTGCTGAGACCTGCGCATCTTGATATGCTGCTTC 604
DB 1293 GGCAGGGTGGTCCCGGGCCGGGCACTCTGCTGAGACCTGCGCATCTTGATATGCTGCTTC 1352
QY 605 CTGCTGTCCAGGTGGCCCATCTCTGTTATGGGCTCCATTGTCAGGCTCAGCCAGTCT 664
DB 1353 CTGCTGTCCAGGTGGCCCATCTCTGTTATGGGCTCCATTGTCAGGCTCAGCCAGTCT 1412
QY 665 GTCACTGCTAATATGATGCTGCGCAGAGCCTGGGTCTGGTGGCCATTACTTGGCTACA 724
DB 1413 GTCACTGCTAATATGATGCTGCGCAGAGCCTGGGTCTGGTGGCCATTACTTGGCTACA 1472
QY 725 CAGGTATGATTTGACAAAGAGCACTTGGCCAAATATCTCAGCGTATGAAAATTTCAGACA 784
DB 1473 CAGGTATGATTTGACAAAGAGCACTTGGCCAAATATCTCAGCGTATGAAAATTTCAGACA 1532
QY 785 TTGGGGTGGAGGGCTGCTCACTGGGTCCAGCTCCCGCTCTGTTAGCCCATGGGG 844
DB 1533 TTGGGGTGGAGGGCTGCTCACTGGGTCCAGCTCCCGCTCTGTTAGCCCATGGGG 1592
QY 845 CTGCCGGGCTGGCCCGCAGTCTTGTGCTGCGCAAGTATGAGTCTCTGTGCTGACCC 904
DB 1593 CTGCCGGGCTGGCCCGCAGTCTTGTGCTGCGCAAGTATGAGTCTCTGTGCTGACCC 1652
QY 905 CTGTGCTGCTGAGTGGCGGTATGCTGCAAGCTGGGGCTGGGGCTGCTCTCTCTCTCC 964
DB 1653 CTGTGCTGCTGAGTGGCGGTATGCTGCAAGCTGGGGCTGGGGCTGCTCTCTCTCTCC 1712
QY 965 CCAAGTCTAGGGGCTGCTGACTGAGAGGCTTCCAGGGGGTTTCACTGAGCTTATAC 1024
```

```
DB 1713 CCAAGTCTAGGGGCTGCTGACTGAGAGGCTTCCAGGGGGTTTCACTGAGCTTATAC 1772
QY 1025 AGGAGGCCAGAAAGGCTTCATGCACTGAAATGCGGGGACTGTGCAAGTGAATACCAG 1084
DB 1773 AGGAGGCCAGAAAGGCTTCATGCACTGAAATGCGGGGACTGTGCAAGTGAATACCAG 1832
QY 1085 GCTCAGGGTTAAACAGTACGCTCCCTTAAGTGAAGACACCTCAGGAAGGGTTTTGGAGC 1144
DB 1833 GCTCAGGGTTAAACAGTACGCTCCCTTAAGTGAAGACACCTCAGGAAGGGTTTTGGAGC 1892
QY 1145 TGAATTAACCTCAGTCACTGTTTCCCATCTGTAAGCCCTTAACCTGAGCTTCCGTTA 1204
DB 1893 TGAATTAACCTCAGTCACTGTTTCCCATCTGTAAGCCCTTAACCTGAGCTTCCGTTA 1952
QY 1205 ATGTAGCTCTTGATGAGGAGTTTCTAGATGAAACATCTCTCATGGAATTTGAACATAT 1264
DB 1953 ATGTAGCTCTTGATGAGGAGTTTCTAGATGAAACATCTCTCATGGAATTTGAACATAT 2012
QY 1265 GAAAGTTATTTGAGGGGGAAGAGTCTGAGGGGCAACACAAAGAACAGGTCCTCCAG 1324
DB 2013 GAAAGTTATTTGAGGGGGAAGAGTCTGAGGGGCAACACAAAGAACAGGTCCTCCAG 2072
QY 1325 CCCACAGCACTGCTTCTTGTGATGATCAACCCCTCTTACTTCTTATCAGAGATGGGCT 1384
DB 2073 CCCACAGCACTGCTTCTTGTGATGATCAACCCCTCTTACTTCTTATCAGAGATGGGCT 2132
QY 1385 GTTGTCTCTTCTGTTGCTATCAACAGACACAGGCAATTAATATTTAATTTATTTATTT 1444
DB 2133 GTTGTCTCTTCTGTTGCTATCAACAGACACAGGCAATTAATATTTAATTTAATTTATTT 2192
QY 1445 AACAAAGTGAAGGGAATCATTGCTAGCTTTCTGTGTGCTATATTTGGGTG 1504
DB 2193 AACAAAGTGAAGGGAATCATTGCTAGCTTTCTGTGTGCTATATTTGGGTG 2252
QY 1505 GGTGGGGATCCCAACAATCAGGTCCCTGAGATGCTGTCATTGGGCTGATCAATTC 1564
DB 2253 GGTGGGGATCCCAACAATCAGGTCCCTGAGATGCTGTCATTGGGCTGATCAATTC 2312
QY 1565 CAGATCTTCTTCTCTGGGGTCTGGCCGCCCAAAATGCTTAAACCAAGACCTTGAAT 1624
DB 2313 CAGATCTTCTTCTCTGGGGTCTGGCCGCCCAAAATGCTTAAACCAAGACCTTGAAT 2372
QY 1625 TCTACTCATCCCAAAATGATTAATCCAAATGCTTAAACCAAGGTTAGGGTTGAAGGA 1684
DB 2373 TCTACTCATCCCAAAATGATTAATCCAAATGCTTAAACCAAGGTTAGGGTTGAAGGA 2432
QY 1685 GGTAGAGGTGGGGCTTCAAGTCTCAACGGCTTCCCTAACCAACCCCTCTTCTTGGGCC 1744
DB 2433 GGTAGAGGTGGGGCTTCAAGTCTCAACGGCTTCCCTAACCAACCCCTCTTCTTGGGCC 2492
QY 1745 AGCTGGTTCCTCCCACTTCACTCCCTCTTACTCTCTAGAGACTGGGCTGATGAAGC 1804
DB 2493 AGCTGGTTCCTCCCACTTCACTCCCTCTTACTCTCTAGAGACTGGGCTGATGAAGC 2552
QY 1805 ACTGCCAAATTTCCCTCAACCCCAAACTTCCCTCAACCCCAAACTTCCCAACGAGCTC 1864
DB 2553 ACTGCCAAATTTCCCTCAACCCCAAACTTCCCTCAACCCCAAACTTCCCAACGAGCTC 2612
QY 1865 CACAAACCTGTTTGGAGTACTGACAGAACCAAGAACCAAGTGCAGTTCACAGCTT 1924
DB 2613 CACAAACCTGTTTGGAGTACTGACAGAACCAAGAACCAAGTGCAGTTCACAGCTT 2672
QY 1925 TGTCAATCTCAGCCCTCAGAGTATCTGTGCTTGGGGAATCTCACAGAAATCAGAGA 1984
DB 2673 TGTCAATCTCAGCCCTCAGAGTATCTGTGCTTGGGGAATCTCACAGAAATCAGAGA 2732
QY 1985 GCAACCCCTGCTGAGCTAAGGAGGCTTATCTCTCAGGGGGGTTTAAGGCGTTTG 2044
DB 2733 GCAACCCCTGCTGAGCTAAGGAGGCTTATCTCTCAGGGGGGTTTAAGGCGTTTG 2792
QY 2045 CATAATGTCGCTTATTTATTTAGCGGGGTAATTTTATATCTGAAGTGAAGCAATCA 2104
DB 2793 CATAATGTCGCTTATTTATTTAGCGGGGTAATTTTATATCTGAAGTGAAGCAATCA 2852
```

QY 2105 GAGTATATGTTTATGTCAGCAAAATTAAGGCTTTCTTATATGTTTA 2152
DB 2853 GAGTATATGTTTATGTCAGCAAAATTAAGGCTTTCTTATATGTTTA 2900

RESULT 6
AR564089
LOCUS AR564089 2904 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 703 from patent US 6759515.
ACCESSION AR564089
VERSION AR564089.1 GI:53979140
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 2904)
Xu J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Kairos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W.,
Hepler, W.T. and Henderson, R.A.
Compositions and methods for the therapy and diagnosis of prostate
cancer
Patent: US 6759515-A 703 06-JUL-2004;
Location/Qualifiers
1..2904
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 97.0%; Score 2088; DB 6; Length 2904;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2088; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 GGCCTTGGAATGGCAGCCTGGGCTGCTCTGCAAGGCGCATCCCGTCTCTCT 124
DB 813 GGGCTTGGAATGGCAGCCTGGGCTGCTCTGCAAGGCGCATCCCGTCTCTCT 872

QY 125 CTGCTCATGACCGGCTGCTGTCAGCGATTCGCACTTGACAGCTTAATTGGCAGTGTG 184
DB 873 CTGCTCATGACCGGCTGCTGTCAGCGATTCGCACTTGACAGCTTAATTGGCAGTGTG 932

QY 185 GCAAGCTTCCCTGCTGCTGCGGTCGCAATGCTGCTCCACAGTGTGGCGCTGTG 244
DB 933 GCAAGCTTCCCTGCTGCTGCGGTCGCAATGCTGCTCCACAGTGTGGCGCTGTG 992

QY 245 GCTTCAAGCGGCTCTCAACCGGCTTCACTTCTCAAGCCCTGCAATCTGCGCTACACATG 304
DB 993 GCTTCAAGCGGCTCTCAACCGGCTTCACTTCTCAAGCCCTGCAATCTGCGCTACACATG 1052

QY 305 GCCTCCCTCTACCAACGGGAGAGAGGCTTCTGCGCCCAATACCGAGGGGACACTGGA 364
DB 1053 GCCTCCCTCTACCAACGGGAGAGAGGCTTCTGCGCCCAATACCGAGGGGACACTGGA 1112

QY 365 GGTGCTAGAGAGAGAGAGAGCTGATGACAGCTTCTGCGAGGCTTAAGCTTGAAGCT 424
DB 1113 GGTGCTAGAGAGAGAGAGAGCTGATGACAGCTTCTGCGAGGCTTAAGCTTGAAGCT 1172

QY 425 CCCTTCCCTAATAGACACGTGGGTGCTGAGGAGAGTGGCTGCTCCACCTTCAACCGCG 484
DB 1173 CCCTTCCCTAATAGACACGTGGGTGCTGAGGAGAGTGGCTGCTCCACCTTCAACCGCG 1232

QY 485 CTTCGCGGGGCTCTGCGCTGATGCTCCGTAAGTGTGAGGAGGAGGAGCCCAACCGAG 544
DB 1233 CTTCGCGGGGCTCTGCGCTGATGCTCCGTAAGTGTGAGGAGGAGGAGCCCAACCGAG 1292

QY 545 GCCAGGAGGCTTCCGGGCGCGGAGCATCTGCTGCACTTGGCATCTTGATAGTGGCTTC 604
DB 1293 GCCAGGAGGCTTCCGGGCGCGGAGCATCTGCTGCACTTGGCATCTTGATAGTGGCTTC 1352

QY 605 CTGCTGCTCCAGAGTGGCGCCATCCCTGTTTATGAGGCTCCATTTGCCAGCTCAGCAAGTCT 664
DB 1353 CTGCTGCTCCAGAGTGGCGCCATCCCTGTTTATGAGGCTCCATTTGCCAGCTCAGCAAGTCT 1412

QY 665 GTCACCTGCCATATATGAGTGTCTGCGCGAGGCTGGGCTCTGCTGCCATTTACTTTGCTACA 724
DB 1413 GTCACCTGCCATATATGAGTGTCTGCGCGAGGCTGGGCTCTGCTGCCATTTACTTTGCTACA 1472

QY 725 CAGGTAGTATTTGACAAAGAGCAGCTTGGCCAAATACTACGCTAGAGAAACCTTCCAGACCA 784
DB 1473 CAGGTAGTATTTGACAAAGAGCAGCTTGGCCAAATACTACGCTAGAGAAACCTTCCAGACCA 1532

QY 785 TTGGGGTGGAGGGGCTGCTCACTGGGTCCTCCAGCTTCCCGCTCTGTTAGCCCAATGGGG 844
DB 1533 TTGGGGTGGAGGGGCTGCTCACTGGGTCCTCCAGCTTCCCGCTCTGTTAGCCCAATGGGG 1592

QY 845 CTGCCGGGCTGGCGCCAGTCTCTGCTGCGCAAGTAATGTGCTCTGCTGCCAC 904
DB 1593 CTGCCGGGCTGGCGCCAGTCTCTGCTGCGCAAGTAATGTGCTCTGCTGCCAC 1652

QY 905 CTGCTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 964
DB 1653 CTGCTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1712

QY 965 CCAGTCTCTAGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1024
DB 1713 CCAGTCTCTAGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1772

QY 1025 AGGAGGCGCAAGAGGCTCCATGCACTGGAATGCGGGGACTCTGCAAGTGTATACCAAG 1084
DB 1773 AGGAGGCGCAAGAGGCTCCATGCACTGGAATGCGGGGACTCTGCAAGTGTATACCAAG 1832

QY 1085 GCTCAGGCTTAAACAGCTAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1144
DB 1833 GCTCAGGCTTAAACAGCTAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1892

QY 1145 TGAATTAACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1204
DB 1893 TGAATTAACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1952

QY 1205 ATGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1264
DB 1953 ATGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2012

QY 1265 GAAAGTATTTGAGAGGAGAGCTGCTGAGAGGAGCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1324
DB 2013 GAAAGTATTTGAGAGGAGAGCTGCTGAGAGGAGCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAG 2072

QY 1325 CCCACAGACCTGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1384
DB 2073 CCCACAGACCTGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2132

QY 1385 GTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1444
DB 2133 GTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2192

QY 1445 AACAAAGTGAAGAGGAATCATTTGCTAGCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1504
DB 2193 AACAAAGTGAAGAGGAATCATTTGCTAGCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2252

QY 1505 GGTGGGGAGATCCCAACATCAAGTCCCTGAGATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1564
DB 2253 GGTGGGGAGATCCCAACATCAAGTCCCTGAGATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2312

QY 1565 CAGAACTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1624
DB 2313 CAGAACTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2372

QY 1625 TCTACTCATCCCAATATGATTAATTTCAATAGCTGTTTACCAAGTGTGAGGAGTGAAGAA 1684
DB 2373 TCTACTCATCCCAATATGATTAATTTCAATAGCTGTTTACCAAGTGTGAGGAGTGAAGAA 2432

QY 1685 GGTAGAGGCTGGGCTTCAAGTCTCAAGGCTTCCCTAAGCAAGGCTCTTCTGCTGGGCC 1744
DB 2433 GGTAGAGGCTGGGCTTCAAGTCTCAAGGCTTCCCTAAGCAAGGCTCTTCTGCTGGGCC 2492

Qy	1745	AGCCGTGTTCCCCCACCATTTCACATCCCTCTACTCTCTCTAGAGACTGGGCTGATGAAGC	1804
Db	2493	AGCCGTGTTCCCCCACCATTTCACATCCCTCTACTCTCTCTAGAGACTGGGCTGATGAAGC	2552
Qy	1805	ACTGCCAAATTTTCCCTTACCCCCCACTTTCCCTTACCCCCCACTTTCCCAACAGCTC	1864
Db	2553	ACTGCCAAATTTTCCCTTACCCCCCACTTTCCCTTACCCCCCACTTTCCCAACAGCTC	2612
Qy	1865	CACAACTCTGTTTGAGGACTGTGCAGACCAAGAACAAAGTCGGGTTTCCACAGCTT	1924
Db	2613	CACAACTCTGTTTGAGGACTGTGCAGACCAAGAACAAAGTCGGGTTTCCACAGCTT	2672
Qy	1925	TGTCATTTCAAGCCCCCAGAGATATCTGTGCTTTGGGGAATCTCACAGAACTCAGGA	1988
Db	2673	TGTCATTTCAAGCCCCCAGAGATATCTGTGCTTTGGGGAATCTCACAGAACTCAGGA	2732
Qy	1985	GCACCCCTGCTGAGCTAAGGAGAGCTCTTATCTCAGGGGGGTTTAAAGCCGTTG	2044
Db	2733	GCACCCCTGCTGAGCTAAGGAGAGCTCTTATCTCAGGGGGGTTTAAAGCCGTTG	2792
Qy	2045	CAATTAATGTCCTTATTTATTTAAAGGGGTGAATATTTTACTGTAAAGTACATCA	2104
Db	2793	CAATTAATGTCCTTATTTATTTAAAGGGGTGAATATTTTACTGTAAAGTACATCA	2852
Qy	2105	GAGTAAATGTTTATGTGACAAATTAAGGCTTCTTAAATGTGTA	2152
Db	2853	GAGTAAATGTTTATGTGACAAATTAAGGCTTCTTAAATGTGTA	2900

RESULT 7			
LOCUS	AX200994	2904 bp	DNA
DEFINITION	Sequence 624 from Patent WO0151633.		
ACCESSION	AX200994		linear
VERSION	AX200994.1	GI:15390821	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		

REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	SOURCE
1	Xu, J., Dillon, D. C., Micham, J. L., Harlocker, S. L., Jiang, Y., Reed, S. G., Kelos, M. D., Fanger, G. R., Day, C. H., Retter, M. W., Stolk, J. A., Skelky, Y. A., Wang, A., and Mesgher, M. J.	Compositions and methods for the therapy and diagnosis of prostate cancer	Patent: WO 0151633-A 624 19-Jul-2001; CORIAX CORPORATION (US)	Location/Qualifiers	I. .2904

11

	Query Match	97.0%;	Score 2088;	DB 6;	Length 2904;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 2088;	Conservative	0;	Mismatches	0;
				Indels	Gaps
Qy	65	GGCGTTGGATGGGCGAGCCTTG3GGCTGTTCCTGCAGTGCAGCCATCTCCCTG3TCTTCTCT	124		
Db	813	GGCGTTCCGAATGGGCGAGCCTTG3GGCTGTTCCTGCAGTGCAGCCATCTCCCTG3TCTTCTCT	872		
Qy	125	CTGGTCATGAGACCGGCTGTCAGCGATTGCGCACTCGAGCAGTCTATTG3CCAGTGTG	184		
Db	873	CTGGTCATGAGACCGGCTGTCAGCGATTGCGCACTCGAGCAGTCTATTG3CCAGTGTG	932		
Qy	185	GCAGTTTCCCTGTGTGGCTGGCCGAGTCCCAATGCTGTCTCCCAAGTGTG3CCGTGTGTACA	244		
Db	933	GCAGTTTCCCTGTGTGGCTGGCCGAGTCCCAATGCTGTCTCCCAAGTGTG3CCGTGTGTACA	992		
Qy	245	GCATTACGCGGCCCTTACCCGGGTTCACTTCTCAGCCCTGCAGATCTG3CCCTACACACTG	304		

Db	993	GCTTCAGCCGCCCTCACCAGGTTACCTTCTCAGCCCTCGACAGATCTGACCCTTACACTG	1052
QY	305	GCCTCCCTCTACCAACCGGAGAAAGCAGGTGTCTCGCCCAATACCGAGGGAGACCTGGA	364
Db	1053	GCCTCCCTCTACCAACCGGAGAAAGCAGGTGTCTCGCCCAATACCGAGGGAGACCTGGA	1112
QY	365	GCTGCTACAGTAGAGAACGCTTGATGACCAAGCTTCTGCGAGGCCCTTAAGCTGAGCT	424
Db	1113	GGTGTACACAGTAGAGAACAGCCTGATGACCAAGCTTCTGCGAGGCCCTTAAGCTGAGCT	1172
QY	425	CCCTTCCCTAATGAGCAAGTAGGGGTCTGGAAGGACAGTGGCCGTCGCCACCTCCACCCGCG	484
Db	1173	CCCTTCCCTAATGAGCAAGTAGGGGTCTGGAAGGACAGTGGCCGTCGCCACCTCCACCCGCG	1232
QY	485	CTCTGCGGGGCTCTGCTCTGATGTCTCCGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGT	544
Db	1233	CTCTGCGGGGCTCTGCTCTGATGTCTCCGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1292
QY	545	GCCAGGGTGTTCGCGGCGCGGGGACCTGCTGCACTCGCCATCTGGAATGTGCTTC	604
Db	1293	GCCAGGGTGTTCGCGGCGCGGGGACCTGCTGCACTCGCCATCTGGAATGTGCTTC	1352
QY	605	CTGCTGTCCCAAGGTGTGCCCCCATCTCCGTGTTATGSGGCTCCATGTGTCAGCTACAGCT	664
Db	1353	CTGCTGTCCCAAGGTGTGCCCCCATCTCCGTGTTATGSGGCTCCATGTGTCAGCTACAGCT	1412
QY	665	GTCACCTGCTTATGTGTGTCTGCGCAGAGGCTGAGGTCTGTGTGTGTCATTTACTTTGCTACA	724
Db	1413	GTCACCTGCTTATGTGTGTCTGCGCAGAGGCTGAGGTCTGTGTGTGTCATTTACTTTGCTACA	1472
QY	725	CAGGTAGTATTTGACAAAGAGGACCTTGCCAAATACTCAGCGTGAAGAAACTTCAGACACA	784
Db	1473	CAGGTAGTATTTGACAAAGAGGACCTTGCCAAATACTCAGCGTGAAGAAACTTCAGACACA	1532
QY	785	TTGGGGGTGAGAGGCGCTGCTACACGTGGGTCCACGTCCCGCTCTCTGTATAGCCCATAGGG	844
Db	1533	TTGGGGGTGAGAGGCGCTGCTACACGTGGGTCCACGTCCCGCTCTCTGTATAGCCCATAGGG	1592
QY	845	CTGCCCGGGCTGAGCGGACAGTTCTGTGTGCTGCCAAAGTAAATGTGGCTCTGCTGCGCAC	904
Db	1593	CTGCCCGGGCTGAGCGGACAGTTCTGTGTGCTGCCAAAGTAAATGTGGCTCTGCTGCGCAC	1653
QY	905	CTGTGTGCTGAGGTGCGTAGCTGCAACAGCTGGGGGCTGGGGCGTCCCTCTCTCTCTCC	964
Db	1653	CTGTGTGCTGAGGTGCGTAGCTGCAACAGCTGGGGGCTGGGGCGTCCCTCTCTCTCTCC	1712
QY	965	CCAAGTCTTACGGGCTGCTGACTGACGTGAGGCTTCCAAAGGGGGTTTCAAGTCTGACTTATAC	1024
Db	1713	CCAAGTCTTACGGGCTGCTGACTGACGTGAGGCTTCCAAAGGGGGTTTCAAGTCTGACTTATAC	1772
QY	1025	AGGAGGCGCAGAAAGGGCTCCATGCACTGGAAATGCGGGGACTCTGCAAGGTGATTAACCA	1084
Db	1773	AGGAGGCGCAGAAAGGGCTCCATGCACTGGAAATGCGGGGACTCTGCAAGGTGATTAACCA	1832
QY	1085	GCTCAGGGTTAAACAGCTAGCCTCTCTAGTTGAGACACACTTAGAAGGGTTTTGGAGC	1144
Db	1833	GCTCAGGGTTAAACAGCTAGCCTCTCTAGTTGAGACACACTTAGAAGGGTTTTGGAGC	1892
QY	1145	TGAATTAACCTAGTCACTGTGTTCCACTCTCTAAGCCCTTAACTCTGACCTTGTTA	1204
Db	1893	TGAATTAACCTAGTCACTGTGTTCCACTCTCTAAGCCCTTAACTCTGACCTTGTTA	1952
QY	1205	ATGATAGCTCTGCAATGGAGGTTTTCAGGATGAAACACTCTCCACATGGGATTTGAAACAT	1264
Db	1953	ATGATAGCTCTGCAATGGAGGTTTTCAGGATGAAACACTCTCCACATGGGATTTGAAACAT	2012
QY	1265	GAAAGTTATTTGTAGGGGAGAGTCTGAGGGGCAACACAAGAACAGAGTCCCTCAG	1324
Db	2013	GAAAGTTATTTGTAGGGGAGAGTCTGAGGGGCAACACAAGAACAGAGTCCCTCAG	2072
QY	1335	CCCAACAGCACTGTCTTTTGTCTGATCCACCCCTCTTACTTTTATCAGAGTGTGCT	1384
Db	2073	CCCAACAGCACTGTCTTTTGTCTGATCCACCCCTCTTACTTTTATCAGAGTGTGCT	2132

OY	1385	GTTGGTCCCTTCGTTGCCATCAACAAGACAGCGCATTTAAATATTACTTATTATT	14		
Db	2133	GTTGGTCCCTTCGTTGCCATCAACAAGACAGCGCATTTAAATATTACTTATTATT	21		
OY	1445	AACAAAGTAGAAGGAATCCATTGTCTACTCTTTCTGTGTGGTGCTAAATATTGGGTAG	15		
Db	2193	AACAAAGTAGAAGGAATCCATTGTCTACTCTTTCTGTGTGGTGCTAAATATTGGGTAG	22		
OY	1505	GATGGGGGATCCCCAACATCAGATCCCCTGAGATAGTGGTCAATTGGGCTGATCATTC	16		
Db	2253	GATGGGGGATCCCCAACATCAGATCCCCTGAGATAGTGGTCAATTGGGCTGATCATTC	23		
OY	1565	CAGAATCTTCTTCTCTGGGGTCTGGCCCCCAAATGCTCTAACCCAGAGACTTGGAAAT	17		
Db	2313	CAGAATCTTCTTCTCTGGGGTCTGGCCCCCAAATGCTCTAACCCAGAGACTTGGAAAT	24		
OY	1625	TCTACTCATCCCAATAATTAATTCCTCAATGCTGTACCAGAGTTAAGGTGTGAAGAA	18		
Db	2373	TCTACTCATCCCAATAATTAATTCCTCAATGCTGTACCAGAGTTAAGGTGTGAAGAA	25		
OY	1685	GGTAGAGGTGGGGCTTCAGGTCTCAACGGCTTCCCTAACACCCCTCTCTGTGGCCC	19		
Db	2433	GGTAGAGGTGGGGCTTCAGGTCTCAACGGCTTCCCTAACACCCCTCTCTGTGGCCC	26		
OY	1745	AGCCTGGTTCCTCCCACTTTCACCTCCCTCTACTCTCTCTAGGACTGGGCTGTAAGGC	20		
Db	2493	AGCCTGGTTCCTCCCACTTTCACCTCCCTCTACTCTCTCTAGGACTGGGCTGTAAGGC	27		
OY	1805	ACTGCCCAAAATTTCCCTACCCCACTTTCCTCCCTACCCCACTTTCCTCCCAAGCTC	21		
Db	2553	ACTGCCCAAAATTTCCCTACCCCACTTTCCTCCCTACCCCACTTTCCTCCCAAGCTC	28		
OY	1865	CACAACCTGTTTGGAGCTACTGACAGACCAAGACCAAAAGTGGGTTTTCCCAAGCTT	22		
Db	2613	CACAACCTGTTTGGAGCTACTGACAGACCAAGACCAAAAGTGGGTTTTCCCAAGCTT	29		
OY	1925	TGTCATCTCAGCCCCAGAGTATCTGTGCTTGGGGAATCTCACACGAATCTACAGA	198		
Db	2673	TGTCATCTCAGCCCCAGAGTATCTGTGCTTGGGGAATCTCACACGAATCTACAGA	273		
OY	1985	GCACCCCCTGCTGAGCTAAGGAGGCTTTATCTCAGGGGGGTTTTAAGTCCGTTTG	204		
Db	2733	GCACCCCCTGCTGAGCTAAGGAGGCTTTATCTCAGGGGGGTTTTAAGTCCGTTTG	279		
OY	2045	CAATATGTCGTTTATTATTATTAAGGGGGTGAATTTTATACGTATGACGATCA	210		
Db	2793	CAATATGTCGTTTATTATTATTAAGGGGGTGAATTTTATACGTATGACGATCA	285		
OY	2105	GAGTATATGTTTATGTCACAAAATTAAGGCTTTCTATATGTTTTA	2152		
Db	2853	GAGTATATGTTTATGTCACAAAATTAAGGCTTTCTATATGTTTTA	2900		
RESULT 8	AX267729	2904 bp	DNA	linear	PAT 26-OCT-2001
LOCUS	AX267729				
DEFINITION	Sequence 703 from Patent WO0170302.				
ACCESSION	AX267729				
VERSION	AX267729.1				
KEYWORDS	GI:16516401				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butleria; Primates; Catarrhini; Hominiidae; Homo.				
REFERENCE	Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Veevick,T.S., Carter,D., Li,S.X., Wang,A., Sketky,Y.A., Hepler,W.T. and Henderson,R.A.				
AUTHORS	Compositions and methods for the therapy and diagnosis of prostate cancer.				
TITLE	Patent: WO 0170302-A 703 04-OCT-2001;				
JOURNAL					

FEATURES	CORIXA CORPORATION (US)
source	location/Qualifiers
	1..2904
	/organism="Homo sapiens"
	/mol_type="unassigned DNA"
	/db_xref="taxon:9606"
ORIGIN	
Query Match	97.0%; Score 2088; DB 6; Length 2904;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 2088; Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY	65 GGGGTTCCGATGAGGAGACCCCTGGGCTGTTCTGTCAGATGCGGCATCTCCCTGGCTTTCTCT
Db	813 GGGGTTCCGATGAGGAGACCCCTGGGCTGTTCTGTCAGATGCGGCATCTCCCTGGCTTTCTCT
QY	125 CTGTCATGAGACCGGCTGGTGTGACAGCATTCGCGCATCTCGAGCAGTCTATTGTCAGATGTG
Db	873 CTGTCATGAGACCGGCTGGTGTGACAGCATTCGCGCATCTCGAGCAGTCTATTGTCAGATGTG
QY	185 GCAGCTTTCCTGTGAGCTCCGAGTGCACATGCTGTCCTCCACAGTGTGGCCGTGTGACA
Db	933 GCAGCTTTCCTGTGAGCTCCGAGTGCACATGCTGTCCTCCACAGTGTGGCCGTGTGACA
QY	245 GCTTCAGCCGCTCTCACCCGGTTCACTTCTCAGCTTCGAGATCTGCCCTTACACACTG
Db	993 GCTTCAGCCGCTCTCACCCGGTTCACTTCTCAGCTTCGAGATCTGCCCTTACACACTG
QY	305 GCCTCCCTTACACACCGGAGAAAGAGGTTTCCTGCCCAATACCGAGGGGACACTGGA
Db	1053 GCCTCCCTTACACACCGGAGAAAGAGGTTTCCTGCCCAATACCGAGGGGACACTGGA
QY	365 GGTGCTAGCAGTGAAGACAGCTTGTGACACAGCTTCTCCAGAGCCCTTACAGCTGAGCT
Db	1113 GGTGCTAGCAGTGAAGACAGCTTGTGACACAGCTTCTCCAGAGCCCTTACAGCTGAGCT
QY	425 CCCTTCCCTTAATGAGACAGTGGGTGTGTCGAGAGCAGTGGCTTCCTCCACTTCACCCGCG
Db	1173 CCCTTCCCTTAATGAGACAGTGGGTGTGTCGAGAGCAGTGGCTTCCTCCACTTCACCCGCG
QY	485 CTCTCCGAGGCTCTGCTCTGATGTCTCCCTAAGTGTGATGTGTGAGGAGCCACAGAG
Db	1233 CTCTCCGAGGCTCTGCTCTGATGTCTCCCTAAGTGTGATGTGTGAGGAGCCACAGAG
QY	545 GGCAGAGGAGTTCGCGGCGCGGGGCAATCTGCTGCACTCGCATCTCGAATAGTGCCTTC
Db	1293 GGCAGAGGAGTTCGCGGCGCGGGGCAATCTGCTGCACTCGCATCTCGAATAGTGCCTTC
QY	605 CTGCTGTCCAGATGTGAGCCCATCCCTGTTTATGAGGCTCAATTGTCAGAGTCAAGCAATCT
Db	1353 CTGCTGTCCAGATGTGAGCCCATCCCTGTTTATGAGGCTCAATTGTCAGAGTCAAGCAATCT
QY	665 GTCACCTGCTTATGATGTGTCTGCGGCAAGGCTGAGTCTGATGCGCATTTACTTTGCTACA
Db	1413 GTCACCTGCTTATGATGTGTCTGCGGCAAGGCTGAGTCTGATGCGCATTTACTTTGCTACA
QY	725 CAGGTAGATTGTCACAGAGGCACTTGGCCCAATATCTCAGAGTGAAGAAATTTCACAGACA
Db	1473 CAGGTAGATTGTCACAGAGGCACTTGGCCCAATATCTCAGAGTGAAGAAATTTCACACACA
QY	785 TTGGGGTGAAGAGGCTGCTCACTGAGTCCCAAGCTCCCGCTCTGTATAGCCCATAGGG
Db	1533 TTGGGGTGAAGAGGCTGCTCACTGAGTCCCAAGCTCCCGCTCTGTATAGCCCATAGGG
QY	845 CTGCGCGGAGTGGCGCGCAGTTTCTGTGTGTCGCCAAATGATGTGGCTCTCTGTGTCACCT
Db	1593 CTGCGCGGAGTGGCGCGCAGTTTCTGTGTGTCGCCAAATGATGTGGCTCTCTGTGTCACCT
QY	905 CTGTGCTGTAAGATGTGTAAGCTGACACAGCTGGAGGCTGAGGAGTCTCTCTCTCTCC
Db	1653 CTGTGCTGTAAGATGTGTAAGCTGACACAGCTGGAGGCTGAGGAGTCTCTCTCTCTCTCC
QY	965 CCAAGTCTTAAGGGCTGCTGAGAGGCTTTCACAGAGGGGTTTCACTGTGACATTATAC

```
Db 1713 CCAAGTCTTAGAGGCTGCTGACCTGAGGCTTCCAAAGGGGTTTCAGTCTGACCTTATAC 1772
Qy 1025 AGGAGAGCCAGAAAGGCTCCATGCACTGAAATCGGGGAACTTGCAAGTGGATTACCCAG 1084
Db 1773 AGGAGAGCCAGAAAGGCTCCATGCACTGAAATCGGGGAACTTGCAAGTGGATTACCCAG 1832
Qy 1085 GCTCAGAGGTTAAGCTAGCTCTGTTGAGACACACCTCAGAGGAGGTTTGGAGC 1144
Db 1833 GCTCAGAGGTTAAGCTAGCTCTGTTGAGACACACCTCAGAGGAGGTTTGGAGC 1892
Qy 1145 TGAATAAAGTCAAGTCACTGTTTCCATCTTAAGCCCTTAACCTGACGTTCCGTTA 1204
Db 1893 TGAATAAAGTCAAGTCACTGTTTCCATCTTAAGCCCTTAACCTGACGTTCCGTTA 1952
Qy 1205 ATGTAGCTCTTGATGAGAGGTTCTAGATGAACACCTCTCATGGGATTTGAACATAT 1264
Db 1953 ATGTAGCTCTTGATGAGAGGTTCTAGATGAACACCTCTCATGGGATTTGAACATAT 2012
Qy 1265 GAAAGTTATTTGAGGGGAAAGTCTGAGGGGCAACACAGAACCCAGTCCCTCAG 1324
Db 2013 GAAAGTTATTTGAGGGGAAAGTCTGAGGGGCAACACAGAACCCAGTCCCTCAG 2072
Qy 1325 CCCACAGCACTGCTTTTGGCTGATCCACCCCTCTTAACCTTTATCAGATGAGCCT 1384
Db 2073 CCCACAGCACTGCTTTTGGCTGATCCACCCCTCTTAACCTTTATCAGATGAGCCT 2132
Qy 1385 GTTGGTCTCTTCTGTCGATCACAAGACACAGGCACTTAAATATTAATTTATTT 1444
Db 2133 GTTGGTCTCTTCTGTCGATCACAAGACACAGGCACTTAAATATTAATTTATTT 2192
Qy 1445 AACAAAGTGAAGAGGAATCCATGTAGCTTTCTGTTGTTGTTGTTGTTGTTGTTG 1504
Db 2193 AACAAAGTGAAGAGGAATCCATGTAGCTTTCTGTTGTTGTTGTTGTTGTTGTTG 2252
Qy 1505 GGTGGGGGATCCCAACAAATCAGAGTCCCTGAGATAGCTGATTTGGGCTGATCATTC 1564
Db 2253 GGTGGGGGATCCCAACAAATCAGAGTCCCTGAGATAGCTGATTTGGGCTGATCATTC 2312
Qy 1565 CAGAACTCTTCTCTCTGTTGGGCTGAGCCCAAAATGCTTAAACCAAGACCTTGAANA 1624
Db 2313 CAGAACTCTTCTCTCTGTTGGGCTGAGCCCAAAATGCTTAAACCAAGACCTTGAANA 2372
Qy 1625 TCTACTCATCCCAAGATTAATTCAAATGCTTAAACCAAGTGAAGGTTGAAGGAA 1684
Db 2373 TCTACTCATCCCAAGATTAATTCAAATGCTTAAACCAAGTGAAGGTTGAAGGAA 2432
Qy 1685 GGTAGAGGTTGGGCTTCAAGTCTCAACGGCTTCCCTTAACACCCCTTTCTTGGCC 1744
Db 2433 GGTAGAGGTTGGGCTTCAAGTCTCAACGGCTTCCCTTAACACCCCTTTCTTGGCC 2492
Qy 1745 AGCTGTGTTCCCTCACTTCCCTCTTACTCTCTTGAAGACTGGGCTGATGAAGC 1804
Db 2493 AGCTGTGTTCCCTCACTTCCCTCTTACTCTCTTGAAGACTGGGCTGATGAAGC 2552
Qy 1805 ACTGCCAAATTTCCCTCACTTCCCTCACTTCCCTCACTTCCCTCACTTCCCTCACTC 1864
Db 2553 ACTGCCAAATTTCCCTCACTTCCCTCACTTCCCTCACTTCCCTCACTTCCCTCACTC 2612
Qy 1865 CACAACTCTGTTGAGACTACTGAGAGACCAAGAGCAAAATGCGGTTTCCAAAGCTT 1924
Db 2613 CACAACTCTGTTGAGACTACTGAGAGACCAAGAGCAAAATGCGGTTTCCAAAGCTT 2672
Qy 1925 TGTTCATCTCAGCCCAAGATTAATCTGTTGGGAAATCTCACAAGAACTCAGGA 1984
Db 2673 TGTTCATCTCAGCCCAAGATTAATCTGTTGGGAAATCTCACAAGAACTCAGGA 2732
Qy 1985 GACACCCCTGCGAGCTAAGGAGGCTTAATCTCAGGGGGGTTTAAGTGCCTTTG 2044
Db 2733 GACACCCCTGCGAGCTAAGGAGGCTTAATCTCAGGGGGGTTTAAGTGCCTTTG 2792
Qy 2045 CAATAATGTCGTTTATTTATTTAGCGGGTGAATATTTTATCTGTAAGTGAATCA 2104
```

```
Db 2793 CAATAATGTCGTTTATTTATTTAGCGGGTGAATATTTTATCTGTAAGTGAATCA 2852
Qy 2105 GAGTATTAATGTTATGTTGACAAATTAAGGCTTTCTATATGTTTA 2152
Db 2853 GAGTATTAATGTTATGTTGACAAATTAAGGCTTTCTATATGTTTA 2900

RESULT 9
AX327336
LOCUS AX327336 3320 bp DNA linear PAT 07-JUN-2002
DEFINITION Sequence 1 from Patent WO0181577.
ACCESSION AX327336
VERSION AX327336.1 GI:18097882
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homosapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 Lau T., Lin, R.J., Parkes, D., Parry, G., Schneider, D.W.,
Steindricher, R., van Heut, P.T. and Wu, J.
Dna encoding the proct 03 polypeptide
Patent: WO 0181577-A 1 01-NOV-2001;
SCHERING AKTIEGESELLSCHAFT (DE)

FEATURES
source
1..3320
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
282..1943
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD20424.1"
/db_xref="GI:18097883"
/translation="MVQRLMVSRLRHRKAQLLVNLTFGLEVCIAAGITVYPPLL
EVGVEKEFTWVLGIGPVGLVCLVLSGASDHMGKRYGRRPFIWLSLILSLFL
IPRAGLGLCPDRPLRLALILGLVGLDVGCVCFPLRPLSLDLPDPDHGSOA
VSVVAFMISIGGCLCYTLPAIDMPSALAPVGTGBCIFGLITLITLVAAATLLVA
EBAALGPTPRAPGASPLSPHCCPRRLAARNIGALLPRLHOLCRRPRLRLFLV
AELCSWMLMTFTLFTYDFVGBGLYQGVPRAPGTBARHYDGVAMSLGLFLQAL
SLVPSLVMDRLVQRTAVVLAASVAAFPVAGATCLSHSVAVVVAASALFTGESAL
QLLPTLASLVYRERKQVFLPKRYGTGASDSISMTSFLPEPKGAAPPNGHVGAG
SGLLPPPLPGASACDVSRYVVPETPARVVPKGICLDIALIIDSARLLSQVNASL
FMGSIVQLSGSYATMWSAAGLGLVAITYATQVVDKSLATKYS"

ORIGIN
Query Match 94.3%; Score 2029; DB 6; Length 3320;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2029; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGCTGTACCAAGGGCTGCCAAGACTGAGCCGGGACCGAGGCCGAGACATATGA 60
Db 1175 GGGGCTGTACCAAGGGCTGCCAAGACTGAGCCGGGACCGAGGCCGAGACATATGA 1234
Qy 61 TGAAGGCGTTTCCGATGAGGAGCGCTGGGGCTGTTCCGCAAGTGGGCCATCTCCCTGGCTT 120
Db 1175 GGGGCTGTACCAAGGGCTGCCAAGACTGAGCCGGGACCGAGGCCGAGACATATGA 1234
Qy 1295 GGGGCTGTACCAAGGGCTGCCAAGACTGAGCCGGGACCGAGGCCGAGACATATGA 1354
Db 1235 TGAAGGCGTTTCCGATGAGGAGCGCTGGGGCTGTTCCGCAAGTGGGCCATCTCCCTGGCTT 1294
Qy 121 CTCTGTGATGATGACCGGCTGGTGGAGGATTCGGCACTCGAGCAAGTCAATTTGGCCAG 180
Db 1295 CTCTGTGATGATGACCGGCTGGTGGAGGATTCGGCACTCGAGCAAGTCAATTTGGCCAG 1354
Qy 181 TGTGGCAGCTTTTCCCTGTTGGCTGGCCGCTGACATGCTGTGTCACAGTGTGGCCGTGCT 240
Db 1355 TGTGGCAGCTTTTCCCTGTTGGCTGGCCGCTGACATGCTGTGTCACAGTGTGGCCGTGCT 1414
Qy 241 GACAGCTTCAAGCGGCTCAACCGGGGTTCACTTTCAGGCTCGAGATCTGCGCCCTACAC 300
Db 1415 GACAGCTTCAAGCGGCTCAACCGGGGTTCACTTTCAGGCTCGAGATCTGCGCCCTACAC 1474
Qy 301 ACTGGCCTCCTCTACCAACCGGAGAGGAGTGTCTGTCGCAATACCGAGGGGACAC 360
Db 1475 ACTGGCCTCCTCTACCAACCGGAGAGGAGTGTCTGTCGCAATACCGAGGGGACAC 1534
```

Qy		1441	ATTTAACTGAAGGAAATTCATTTGTAGCTTTCTGTGTGGTGCTAATAATTTGG	1500
Db		2615	ATTTAACAAGTAGAGGAAATCCATTTGTAGCTTTCTGTGTGGTGCTAATAATTTGG	2677
Qy		1501	GTMGGGTGGGGATATCCCACAAATCAATGATGCCCTGAGATAGTGATCATTTGGCTGATCA	1566
Db		2675	GTMGGGTGGGGATATCCCACAAATCAATGATGCCCTGAGATAGTGATCATTTGGCTGATCA	2733
Qy		1561	TTCSCAGAATCTTCTTCTCCTGTGGGGGTGTGGCCCCCAAATGECCTAACCCAGACTTTGG	1622
Db		2735	TTCSCAGAATCTTCTTCTCCTGTGGGGGTGTGGCCCCCAAATGECCTAACCCAGACTTTGG	2794
Qy		1621	AAATTCTACTCATCCCAATGATTAATTCCAATGCTGTATCCCAAGTTAGGGTGTTGA	1680
Db		2795	AAATTCTACTCATCCCAATGATTAATTCCAATGCTGTATCCCAAGTTAGGGTGTTGA	2855
Qy		1681	GGAAGGTAGAGGGTGGGGCTTAGAGTTCACAGCGTTTCCCTTAACCAACCCTTCTTTG	1744
Db		2855	GGAAGGTAGAGGGTGGGGCTTAGAGTTCACAGCGTTTCCCTTAACCAACCCTTCTTTG	2914
Qy		1741	GCCCAAGCTGTATCCGCCCACTTCCACTCCCTCTACTCTCTTAGAGACTGGGCTGATGA	1800
Db		2915	GCCCAAGCTGTATCCGCCCACTTCCACTCCCTCTACTCTCTTAGAGACTGGGCTGATGA	2974
Qy		1801	AAGCACTGGCCAAATTTTCCCTAACCCCAACTTTCCCTAACCCCAACTTTCCCAACA	1860
Db		2975	AAGCACTGGCCAAATTTTCCCTAACCCCAACTTTCCCTAACCCCAACTTTCCCAACA	3034
Qy		1861	GCTCCACAACCTCTGTTTGGAGCTACTGAGAGCACAGAACAAAGTGCGGTTTCCCAAG	1920
Db		3035	GCTCCACAACCTCTGTTTGGAGCTACTGAGAGCACAGAACAAAGTGCGGTTTCCCAAG	3094
Qy		1921	CCTTTGTGCATCTACGCCCCCAAGATATATCTGTGCTTGGGGAATTTTCACACAGAAATC	1980
Db		3095	CCTTTGTGCATCTACGCCCCCAAGATATATCTGTGCTTGGGGAATTTTCACACAGAAATC	3154
Qy		1981	AGAGACACCCCTGCTGAGCTTAAGGAGAGTCTTATCTCTCAGGGGGGG	2029
Db		3155	AGAGACACCCCTGCTGAGCTTAAGGAGAGTCTTATCTCTCAGGGGGGG	3203
RESULT 10				
AR112294				
LOCUS	AR112294	2143 bp	DNA	linear PAT 16-MAY-2001
DEFINITION	Sequence 15 from patent US 6130043.			
ACCESSION	AR112294			
VERSION	AR112294.1 GI:14092194			
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REPERE	Unclassified.			
AUTHORS	1 (bases 1 to 2143)			
	Billing-Wedel, P.A., Cohen, M., Colplite, T.L., Friedman, P.N.,			
	Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D.,			
	Roberts-Kapp, L., Russell, J.C., Stroupe, S.D. and Yu, H.			
	Reagents-kapp, L., Russell, J.C., Stroupe, S.D. and Yu, H.			
	Patient: US 6130043-A 15 10-OCT-2000;			
	Location/Qualifiers			
JOURNAL	1. .2143			
FEATURES	/organism="unknown"			
source	/mol_type="unassigned DNA"			
ORIGIN				
Query Match	91.6%; Score 1972; DB 6; Length 2143;			
Best Local Similarity	99.9%; Pred. No. 0;			
Matches 2142; Conservative	0; Mismatches 1; Indels 1; Gaps 1;			
Qy	9 ACCGAGGCGCTGCCAGAGCTGAGCCGGGCAACGAGGCGCTGGAGACATATGATGAAGCG	68		
Db	1 ACCAGGCGCTGCCAGAGCTGAGCCGGGCAACGAGGCGCTGGAGACATATGATGAAGCG	60		
Qy	69 TTGCGATGGGACCTGGGGCTGTTCTGTGAAGTGGGCATCTCCCTGATTTCTCTTGG	128		

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 4034)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kajos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,M.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6512094-A 704 28-JAN-2003;
FEATURES Location/Qualifiers
Source 1..4034
/organism="unknown"
/mol_type="genomic DNA"

Query Match 91.4%; Score 1968; DB 6; Length 4034;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2088; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 64 AGGCGTTCGATGGGAGCGCTGGGGCTGTCTTCGACATGCGCCATCTCCCTGCTTTCTC 123
Db 1943 AGGCGTTCGATGGGAGCGCTGGGGCTGTCTTCGACATGCGCCATCTCCCTGCTTTCTC 2002
QY 124 TCTGGTCATGAGACCGGCTGTGACGCGATTCGGCACTCGACAGTCTATTGGCCAGTGT 183
Db 2003 TCTGGTCATGAGACCGGCTGTGACGCGATTCGGCACTCGACAGTCTATTGGCCAGTGT 2062
QY 184 GGCAGCTTTCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 243
Db 2063 GGCAGCTTTCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2122
QY 244 AGCTTACGCCCGCTTACCGCGGTTACCTTCTCAGCCCTGACAGATCCTGCGCCCTACACT 303
Db 2123 AGCTTACGCCCGCTTACCGCGGTTACCTTCTCAGCCCTGACAGATCCTGCGCCCTACACT 2182
QY 304 GGGCTTCCCTTACCAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 363
Db 2183 GGGCTTCCCTTACCAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2242
QY 364 AGGTGCTAGCAG 423
Db 2243 AGGTGCTAGCAG 2302
QY 424 TCCCTTCCCTTATGACACGTGGGTCTGAGAGCAGTGGCTGCTCCACTCCACCCGC 483
Db 2303 TCCCTTCCCTTATGACACGTGGGTCTGAGAGCAGTGGCTGCTCCACTCCACCCGC 2362
QY 484 GCTCTGCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 543
Db 2363 GCTCTGCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2422
QY 544 GGCAGAGGTGTGCTTCCGGGCGGGGCGCATCTGCGTGAACCTGCGCATCTGGATAGGCTT 603
Db 2423 GGCAGAGGTGTGCTTCCGGGCGGGGCGCATCTGCGTGAACCTGCGCATCTGGATAGGCTT 2482
QY 604 CCTGCTGTCCCAAGTGGCCCAATCCCTGTTATGAGGCTTCATGTCAGCTCAGCCAGTGC 663
Db 2483 CCTGCTGTCCCAAGTGGCCCAATCCCTGTTATGAGGCTTCATGTCAGCTCAGCCAGTGC 2542
QY 664 TGTCACTGCTATATGAGTGTCTGCGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 723
Db 2543 TGTCACTGCTATATGAGTGTCTGCGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 2602
QY 724 ACAGGTAGTATTGACAAAG 783
Db 2603 ACAGGTAGTATTGACAAAG 2662
QY 784 ATTGGGGTGGAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 843
Db 2663 ATTGGGGTGGAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2722

QY 844 GCTGCCGGGCTGCGCGCCAGATTCTGTGCTGCGCAAGATATGTGGCTCTGCTGCCAC 903
Db 2723 GCTGCCGGGCTGCGCGCCAGATTCTGTGCTGCGCAAGATATGTGGCTCTGCTGCCAC 2782
QY 904 CCTGTGCTGCTAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 963
Db 2783 CCTGTGCTGCTAGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2842
QY 964 CCCAGTCTCTAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1023
Db 2843 CCCAGTCTCTAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2902
QY 1024 CAGGAGGCGCAGAGAGGCTCCATGCACTGGAATGCGGAGACTTGCAGGTGATTAACCA 1083
Db 2903 CAGGAGGCGCAGAGAGGCTCCATGCACTGGAATGCGGAGACTTGCAGGTGATTAACCA 2962
QY 1084 GGCCTAGGGTTAAACAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1143
Db 2963 GGCCTAGGGTTAAACAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3022
QY 1144 CTGAATTAACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1203
Db 3023 CTGAATTAACCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3082
QY 1204 AATGTAGCTCTTGCATGAGGAGTCTTCTAGATGAACACTCTCTCAATGGGATTTGAACATA 1263
Db 3083 AATGTAGCTCTTGCATGAGGAGTCTTCTAGATGAACACTCTCTCAATGGGATTTGAACATA 3142
QY 1264 TGAAGTTATTTGTAAGGGAAGAGTCTGAGGGGCAACACAGAAACAGAGTCCCTCA 1323
Db 3143 TGAAGTTATTTGTAAGGGAAGAGTCTGAGGGGCAACACAGAAACAGAGTCCCTCA 3202
QY 1324 GCCCAGACACTGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1383
Db 3203 GCCCAGACACTGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3261
QY 1384 TGTGTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1443
Db 3262 TGTGTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3321
QY 1444 TAAAGATAGAGAGAGATTCATTGCTAGCTTTTCTGTGTGTGCTGCTGCTGCTGCTGCTG 1503
Db 3322 TAAAGATAGAGAGAGATTCATTGCTAGCTTTTCTGTGTGTGCTGCTGCTGCTGCTGCTG 3381
QY 1504 GGGTGGGGGATCCCAACCAATCAAGTCCCTGAGATGCTGCTGCTGCTGCTGCTGCTGCTG 1563
Db 3382 GGGTGGGGGATCCCAACCAATCAAGTCCCTGAGATGCTGCTGCTGCTGCTGCTGCTGCTG 3441
QY 1564 CCAAGATCTTCTCTCTGCGGGTCTGCGCCCGCCCAAAATGCTTAACCCAGGACCTTGGAAA 1623
Db 3442 CCAAGATCTTCTCTCTGCGGGTCTGCGCCCGCCCAAAATGCTTAACCCAGGACCTTGGAAA 3501
QY 1624 TTTCTACTCATCCCAATGATTAATTCGAATGCTGTTAACCAAGGTTAGGAGTTGAAGA 1683
Db 3502 TTTCTACTCATCCCAATGATTAATTCGAATGCTGTTAACCAAGGTTAGGAGTTGAAGA 3561
QY 1684 AGGTAGAGGGTGGGGCTTCAAGTCTCAAGGCTTCCCTTAACCAACCCCTCTCTTGGGCC 1743
Db 3562 AGGTAGAGGGTGGGGCTTCAAGTCTCAAGGCTTCCCTTAACCAACCCCTCTCTTGGGCC 3621
QY 1744 CAGCTGCTTCCCGCCCACTTCACTCCCTCTACTCTCTAGAGCTGAGGCTGATGAAG 1803
Db 3622 CAGCTGCTTCCCGCCCACTTCACTCCCTCTACTCTCTAGAGCTGAGGCTGATGAAG 3681
QY 1804 CACTGCGCAAAATTTTCCCTTACCCCACTTCCCTTACCCCACTTCCCACTGAGCT 1863
Db 3682 CACTGCGCAAAATTTTCCCTTACCCCACTTCCCTTACCCCACTTCCCACTGAGCT 3741
QY 1864 CCACAAACCTGTTTGAAGCTACTGACAGACAGAAAGCAAAAGTGGGTTTCCCAAGCCT 1923
Db 3742 CCACAAACCTGTTTGAAGCTACTGACAGACAGAAAGCAAAAGTGGGTTTCCCAAGCCT 3801
QY 1924 TTTGTCATCTCAGCCCGCCAGAGATATCTGTGCTTGGGGAATCTCAACAGAAACTCAG 1983

Db 3802 TTCTCATCTCAGCCCCCAGATATCTGTGCTGGGAAATCTCACAGAACTCAGG 3861
QY 1984 AGCACCCTCTGCTGAGCTAAGGAGGCTTATCTCTCAGAGGGGGTTTAAAGCCGTTT 2043
Db 3862 AGCACCCTCTGCTGAGCTAAGGAGGCTTATCTCTCAGAGGGGGTTTAAAGCCGTTT 3921
QY 2044 GCATTAATGCTCTTATTTATTTAAGGGGTAATTTTAACTGTAAGTAAAGCAATC 2103
Db 3922 GCATTAATGCTCTTATTTATTTAAGGGGTAATTTTAACTGTAAGTAAAGCAATC 3981
QY 2104 AGAGTAAATGTTATGATGACAAAATTAAGGCTTCTTATATGTTTA 2152
Db 3982 AGAGTAAATGTTATGATGACAAAATTAAGGCTTCTTATATGTTTA 4030
RESULT 12
AR400443 4034 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 704 from patent US 6620922.
DEFINITION AR400443
ACCESSION AR400443
VERSION AR400443.1 GI:40143820
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4034)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kaleo,M.D., Fanger,G.R., Reiter,M.W., Stolk,J.A., Day,C.H.,
Veddyck,T.S., Carter,D., Li,S.X., Wang,A., Skelley,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITILE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6620922-A 704 16-SEP-2003;
FEATURES
source 1. 4034
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 91.4%; Score 1968; DB 6; Length 4034;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2088; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 64 AGCGCTTCGAGTGGGAGGCTGGGGCTGTTCTGTCAGTGGGCAATCTCCCTGCTTCTC 123
Db 1943 AGCGCTTCGAGTGGGAGGCTGGGGCTGTTCTGTCAGTGGGCAATCTCCCTGCTTCTC 2002
QY 124 TCTGTCATGAGACCGGCTGGTGCAGGATTCGGGACATCGACAGCTATTTGGCCAGTGT 183
Db 2003 TCTGTCATGAGACCGGCTGGTGCAGGATTCGGGACATCGACAGCTATTTGGCCAGTGT 2062
QY 184 GGCAGCTTTCCTGTCGCTGCGGTCGCCATATGCTGTCGCCAGTGGGCGGTGTGAC 243
Db 2063 GGCAGCTTTCCTGTCGCTGCGGTCGCCATATGCTGTCGCCAGTGGGCGGTGTGAC 2122
QY 244 AGCTTCAGCGGCTCTACCGGGTTCACCTTTCAGGCTTCGACAGATCTTGCCCTACACT 303
Db 2123 AGCTTCAGCGGCTCTACCGGGTTCACCTTTCAGGCTTCGACAGATCTTGCCCTACACT 2182
QY 304 GGCCTCCCTCTACCAACGGGAGAGAGAGGTTCCGGCCAAATACGAGGGGACACTGG 363
Db 2183 GGCCTCCCTCTACCAACGGGAGAGAGAGGTTCCGGCCAAATACGAGGGGACACTGG 2242
QY 364 AGGTGCTACAGTGAAGAGACGCTGATGACACAGCTTCTGTCAGGCGCTTAAAGCTGAGC 423
Db 2243 AGGTGCTACAGTGAAGAGACGCTGATGACACAGCTTCTGTCAGGCGCTTAAAGCTGAGC 2302
QY 424 TCCCTTCCCTAATGACAGTGGGTCCTGAGGCAAGTGGCTGCTCCACCTCCACCCG 483
Db 2303 TCCCTTCCCTAATGACAGTGGGTCCTGAGGCAAGTGGGCTGCTCCACCTCCACCCG 2362
QY 484 GGTCTGCGGGGCTCTGCTGTGATGTCTCCGTAAGTGTGGTGGTGAAGCCACCGA 543

Db 2363 GCTCTCGGGGCTCTGCTGTGATGTCTCCGTAAGTGTGGTGAAGCCACCGA 2422
QY 544 GGCAGAGGTGTTCCGGGCGGGGCAATGCTGGAACCTCGCCATCTGGATAGTGCCTT 603
Db 2423 GGCAGAGGTGTTCCGGGCGGGGCAATGCTGGAACCTCGCCATCTGGATAGTGCCTT 2482
QY 604 CCGTCTGTCCCAAGTGGGCCCATCCCTGTTTATGGGCTCATTTGTCACTCAGCTCAGCAATC 663
Db 2483 CCGTCTGTCCCAAGTGGGCCCATCCCTGTTTATGGGCTCATTTGTCACTCAGCTCAGCAATC 2542
QY 664 TGTCACTGCTATATGATGTGTCGCGCAGAGGCTGGGTCGTGTCGACATTTACTTGTCTAC 723
Db 2543 TGTCACTGCTATATGATGTGTCGCGCAGAGGCTGGGTCGTGTCGACATTTACTTGTCTAC 2602
QY 724 ACAGTAGTATTTGACCAAGAGCGACTTGGCCAAATATCTAGCGTAAAGAACTTCAGACAC 783
Db 2603 ACAGTAGTATTTGACCAAGAGCGACTTGGCCAAATATCTAGCGTAAAGAACTTCAGACAC 2662
QY 784 ATTTGGGTGAGAGGCTGCTGCTCACTGAGGTCGCCAGCTCCCGCTCTGTTAGCCCATGGG 843
Db 2663 ATTTGGGTGAGAGGCTGCTGCTCACTGAGGTCGCCAGCTCCCGCTCTGTTAGCCCATGGG 2722
QY 844 GCTGCGGGGCTGGCGGCGCAGTTTCTGTGCTGCAAAAGTAATGTGCTCTGCTGCGCAC 903
Db 2723 GCTGCGGGGCTGGCGGCGCAGTTTCTGTGCTGCAAAAGTAATGTGCTCTGCTGCGCAC 2782
QY 904 CCTGTGCTGCTGAGGTCGCTGAGCTGACAGCTGAGGCTTCCAGAGGGGTTTATGCTGGAATTATA 1023
Db 2783 CCGTGTCTCTGAGGTCGCTGAGCTGACAGCTGAGGCTTCCAGAGGGGTTTATGCTGGAATTATA 2842
QY 964 CCCAGTCTTAGGGCTGCTGCTGACCTGAGGCTTCCAGAGGGGTTTATGCTGGAATTATA 1023
Db 2843 CCCAGTCTTAGGGCTGCTGCTGACCTGAGGCTTCCAGAGGGGTTTATGCTGGAATTATA 2902
QY 1024 CAGGAGGCGCAGAGAGGCTCCATGACCTGGAATGCGGGGACTCTGAGGTTGATTAACCA 1083
Db 2903 CAGGAGGCGCAGAGAGGCTCCATGACCTGGAATGCGGGGACTCTGAGGTTGATTAACCA 2962
QY 1084 GGTCTAGGGTTTAAACAGTACCTCTTATGTTGAGACACACTGAGAGAGGTTTGGGAG 1143
Db 2963 GGTCTAGGGTTTAAACAGTACCTCTTATGTTGAGACACACTGAGAGAGGTTTGGGAG 3022
QY 1144 CTGAATTAATCTGATCACTGCTGTTTCCATCTCTAAGCCCTTAACTGCACTTGTGTT 1203
Db 3023 CTGAATTAATCTGATCACTGCTGTTTCCATCTCTAAGCCCTTAACTGCACTTGTGTT 3082
QY 1204 AATGTAGCTCTTGCATGGAGTTTCTAGAGATGAACACTCTCCATGGGATTTGAACATA 1263
Db 3083 AATGTAGCTCTTGCATGGAGTTTCTAGAGATGAACACTCTCCATGGGATTTGAACATA 3142
QY 1264 TGAAGTTATTTGTAGGGGAGAGTCTTGAGGGGCAACACAGAGAGAGTCCCTCA 1323
Db 3143 TGAAGTTATTTGTAGGGGAGAGTCTTGAGGGGCAACACAGAGAGAGTCCCTCA 3202
QY 1324 GCCCAGACAGCTGCTTTTGTGCTGATCCACCCCTCTTAACTTTTATAGAGTGTGGCC 1383
Db 3203 GCCCAGACAGCTGCTTTTGTGCTGATCCACCCCTCTTAACTTTTATAGAGATGT- GCC 3261
QY 1384 TGTGTGCTCTTGTGTTGTCATGACAGAGACAGAGGATTTAAATTTAACTTATTT 1443
Db 3262 TGTGTGCTCTTGTGTTGTCATGACAGAGACAGAGGATTTAAATTTAACTTATTTAT 3321
QY 1444 TAAACAAGTAGAAGGGAATCAATGCTAGCTTTTCTGTGTGTGTTCTAATATTTGGGTA 1503
Db 3322 TAAACAAGTAGAAGGGAATCAATGCTAGCTTTTCTGTGTGTGTTCTAATATTTGGGTA 3381
QY 1504 GGTGTGGGGAATCCCAACATCAAGTCCCTGATAGATAGTGTGCTATTTGGCTGATCATTTG 1563
Db 3382 GGTGTGGGGAATCCCAACATCAAGTCCCTGATAGATAGTGTGCTATTTGGCTGATCATTTG 3441
QY 1564 CCAGAACTCTTCTTCTGCGGGTGTGGGCCCCCAAAATGCTTAACGACGCTTGGAAA 1623

Db 3442 CCAGATCTTTCTCTCTGAGGCTGCCCCCAAAATCCCTAACCCAGACTTTGAAA 3501
Qy 1624 TTCTACTCATCCCAATATGTAATTCGAATGCTGTTACCAAGTTAGGGTGTGAAGA 1683
Db 3502 TTCTACTCATCCCAATATGTAATTCGAATGCTGTTACCAAGTTAGGGTGTGAAGA 3561
Qy 1684 AGGTAGAGGGTGGGGCTTCAGGCTCAAGGGCTTCCCAACACCCCTCTCTTGGCC 1743
Db 3562 AGGTAGAGGGTGGGGCTTCAGGCTCAAGGGCTTCCCAACACCCCTCTCTTGGCC 3621
Qy 1744 CAGCTGCTTCCCACTTCACTCCCTCTCACTCTCTAGGACTGGGCTGTAAGA 1803
Db 3622 CAGCTGCTTCCCACTTCACTCCCTCTCACTCTCTAGGACTGGGCTGTAAGA 3681
Qy 1804 CAGTGGCCAAATTTCCCTTACCCCACTTCCCTTACCCCACTTCCCACTGCT 1863
Db 3682 CAGTGGCCAAATTTCCCTTACCCCACTTCCCTTACCCCACTTCCCACTGCT 3741
Qy 1864 CCACAACTCTTTGAGCTACTGACAGGACCAAGACCAAAAGTGGGTTCCCAAGCT 1923
Db 3742 CCACAACTCTTTGAGCTACTGACAGGACCAAGACCAAAAGTGGGTTCCCAAGCT 3801
Qy 1924 TTTCCTACTGACGCCCCCAAGTATATCTGCTTGGGAAATCTCACAGAAATCTAG 1983
Db 3802 TTTCCTACTGACGCCCCCAAGTATATCTGCTTGGGAAATCTCACAGAAATCTAG 3861
Qy 1984 AGCAGCCCTGCTGAGCTAAGGAGGCTTATCTCAAGGGGGTTTAAAGTCCGCTT 2043
Db 3862 AGCAGCCCTGCTGAGCTAAGGAGGCTTATCTCAAGGGGGTTTAAAGTCCGCTT 3921
Qy 2044 GCATTAATGCTGCTTATTTATTTTAAAGGGGTAATATTTTATCTGTAAGTGAATC 2103
Db 3922 GCATTAATGCTGCTTATTTATTTTAAAGGGGTAATATTTTATCTGTAAGTGAATC 3981
Qy 2104 AGATTAATGCTTATGTAAGGAAATTAAGGCTTCTTATATGTTTA 2152
Db 3982 AGATTAATGCTTATGTAAGGAAATTAAGGCTTCTTATATGTTTA 4030

RESULT 13
AR405710 4034 bp DNA 1linear PAT 18-DEC-2003
LOCUS Sequence 704 from patent US 6630305.
DEFINITION AR405710
ACCESSION AR405710
VERSION AR405710.1 GI:40154547
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4034)
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harloker, S.L., Jiang, Y., Kado, M.D., Fanger, G.R., Reiter, M.W., Stolk, J.A., Day, C.H., Vedler, T.S., Carter, D., Li, S.X., Wang, A., Skelky, Y.A.W., Hepler, M.T. and Henderson, R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6630305-A 704 07-OCT-2003;
FEATURES
source 1.4034
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 91.4%; Score 168; DB 6; Length 4034;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2088; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 64 AGCGCTTCGATGAGCAGGCTGGGCTGTTCTCTGAGGCGCAATCCCTGCTTCTC 123
Db 1943 AGCGCTTCGATGAGCAGGCTGGGCTGTTCTCTGAGGCGCAATCCCTGCTTCTC 2002
Qy 124 TCTGTCATGACCGGCTGCTGACGCAATTCGCACTGACAGCTATTTGGCAGTGT 183

Db 2003 TCTGTCATGACCGGCTGCTGACGATTCGGCACTGAGAGTCTATTTGGCCAGTGT 2062
Qy 184 GCGAGCTTTCCCTGAGGCTGGCCGCTGACCAATGCTGTTCCCAAGTGGCTGTGAC 243
Db 2063 GCGAGCTTTCCCTGAGGCTGGCCGCTGACCAATGCTGTTCCCAAGTGGCTGTGAC 2122
Qy 244 AGCTTACGCGGCTTCAACCGGGTTCACTTCTCAGCCCTGAGATCTGCTTACACT 303
Db 2123 AGCTTACGCGGCTTCAACCGGGTTCACTTCTCAGCCCTGAGATCTGCTTACACT 2182
Qy 304 GGCCTTCCCTTCAACCGGGAAGACAGGTTTCTGCTCCAAATACGAGGGACACTGG 363
Db 2183 GGCCTTCCCTTCAACCGGGAAGACAGGTTTCTGCTCCAAATACGAGGGACACTGG 2242
Qy 364 AGTGTGACGATGAGACAGGCTGATGACAGTCTTCCGACAGGCTTAAAGCTGAGC 423
Db 2243 AGTGTGACGATGAGACAGGCTGATGACAGTCTTCCGACAGGCTTAAAGCTGAGC 2302
Qy 424 TCCCTTCCCTTAAATGACAGTGGGCTGAGAGGAGGAGGCTGCTCCACCTCCACCCG 483
Db 2303 TCCCTTCCCTTAAATGACAGTGGGCTGAGAGGAGGAGGCTGCTCCACCTCCACCCG 2362
Qy 484 GCTCTGCGGGGCTGCTGCTGATGATGCTCCGTAAGTGGTGGTGGTGAAGCCACGA 543
Db 2363 GCTCTGCGGGGCTGCTGCTGATGATGCTCCGTAAGTGGTGGTGGTGAAGCCACGA 2422
Qy 544 GGCAGAGGTGTTCCGGCCCGGGCAATGCTGCTGACCTCGCANTCTGATAGTGCCT 603
Db 2423 GGCAGAGGTGTTCCGGCCCGGGCAATGCTGCTGACCTCGCANTCTGATAGTGCCT 2482
Qy 604 CCGTCTGCCAGAGTGGCCCAATCCCTGTTTATGGGCTCCATTTGCACTGACGCAATC 663
Db 2483 CCGTCTGCCAGAGTGGCCCAATCCCTGTTTATGGGCTCCATTTGCACTGACGCAATC 2542
Qy 664 TGTCACTGCTATATGATGCTGCTGCGAGGCTGGTCTGGTGGCAATTTACTTGTAC 723
Db 2543 TGTCACTGCTATATGATGCTGCTGCGAGGCTGGTCTGGTGGCAATTTACTTGTAC 2602
Qy 724 ACAGTATATTTTACAAGAGGCACTTGGCCAAATCTACAGCTGAGAAAATTCCAGCAC 783
Db 2603 ACAGTATATTTTACAAGAGGCACTTGGCCAAATCTACAGCTGAGAAAATTCCAGCAC 2662
Qy 784 ATTGGGTTGAGGAGGCTGCTGCTGACCTGGTCCAGCTCCCGCTCCGTTAGCCCATGG 843
Db 2663 ATTGGGTTGAGGAGGCTGCTGCTGACCTGGTCCAGCTCCCGCTCCGTTAGCCCATGG 2722
Qy 844 GCTCCCGGCTGGCGGCACTTCTGTTGCTGCAAGTATGATGCTCTGCTGCGAC 903
Db 2723 GCTCCCGGCTGGCGGCACTTCTGTTGCTGCAAGTATGATGCTCTGCTGCGAC 2782
Qy 904 CCGTGTGCTGAGGAGGCTGAGTGCACAGCTGGGGCTGGGGCTGCTCTCTCTCTC 963
Db 2783 CCGTGTGCTGAGGAGGCTGAGTGCACAGCTGGGGCTGGGGCTGCTCTCTCTCTC 2842
Qy 964 CCGAGTCTTAAAGGCTGCTGACCTGAGGCTTCAAGGGGGTTTCAAGTCTGACTTAA 1023
Db 2843 CCGAGTCTTAAAGGCTGCTGACCTGAGGCTTCAAGGGGGTTTCAAGTCTGACTTAA 2902
Qy 1024 CAGGAGGCGCAAGAGGCTTCACTGACCTGGAATGCGGGGACTCTGAGGTTGACCA 1083
Db 2903 CAGGAGGCGCAAGAGGCTTCACTGACCTGGAATGCGGGGACTCTGAGGTTGACCA 2962
Qy 1084 GGCCTCAGGGTTAACACTAGCTAGCTCCTAGTTGAGACACACTTGAAGAGGTTTGGAG 1143
Db 2963 GGCCTCAGGGTTAACACTAGCTAGCTCCTAGTTGAGACACACTTGAAGAGGTTTGGAG 3022
Qy 1144 CTGAATTAATCACTGACCTGTTCCATCTCTTAAAGCCCTTAACTGCACTTCTGTT 1203
Db 3023 CTGAATTAATCACTGACCTGTTCCATCTCTTAAAGCCCTTAACTGCACTTCTGTT 3082
Qy 1204 AATGTAGCTCTTGAATGGAGTTTCTAAGATGAACACTCTCTCAATGGATTTGAACATA 1263
Db 3083 AATGTAGCTCTTGAATGGAGTTTCTAAGATGAACACTCTCTCAATGGATTTGAACATA 3142

QY	1264	GGAAAGTATTGTATGGGGGAAAGAGCTCTGAAGGGGCAACAACAAGAACACAGGTCCCCCA	1323
Db	3143	TGAAAGTTATTGTATGGGGAAAGAGCTCTGAAGGGGCAACAACAAGAACACAGGTCCCCCA	3202
QY	1324	GCCCAAGACACTGTCTTTTGTGTGATCAACCCCTCTTACCTTTATCAGAGTGTGACC	1383
Db	3203	GCCCAAGACACTGTCTTTTGTGTGATCAACCCCTCTTACCTTTATCAGAGTGTGACC	3261
QY	1384	TGTTGTCTCTTGTGTGATCAACAGGCAATTTAAATTTTAACTTATTTAT	1443
QY	1444	TAAACAAGTAGAAGGAATCCATTGCTAGCTTTTCTGTGTGTGTCTAAATATTGGGTA	1503
Db	3322	TAAACAAGTAGAAGGAATCCATTGCTAGCTTTTCTGTGTGTGTCTAAATATTGGGTA	3381
QY	1504	GGGTGGGGAGATCCCAACAATCAGGTCCCCTGAGATAGCTGTCTATGGGCTGATCAT	1563
Db	3382	GGGTGGGGAGATCCCAACAATCAGGTCCCCTGAGATAGCTGTCTATGGGCTGATCAT	3441
QY	1564	CCAGAAATCTTCTTCTCTGGGGCTGTGGCCCCCAAAATGCGTAAACCCAGAGACTTGGAAA	1623
Db	3442	CCAGAAATCTTCTTCTCTGGGGCTGTGGCCCCCAAAATGCGTAAACCCAGAGACTTGGAAA	3501
QY	1624	TTCTACTCATCCCAAAATGATTAATTCCTGATGCTGTAAACCAAGTTAGGGTGTGGAAGA	1683
Db	3502	TTCTACTCATCCCAAAATGATTAATTCCTGATGCTGTAAACCAAGTTAGGGTGTGGAAGA	3561
QY	1684	AGGTAGAGAGGTGGGGCTTCAGGTCTCAAGGCTTCCCTTAACACACCCCTCTTCTGTGGCC	1743
Db	3562	AGGTAGAGAGGTGGGGCTTCAGGTCTCAAGGCTTCCCTTAACACACCCCTCTTCTGTGGCC	3621
QY	1744	CAGCCTGTGTTCCCCCACTTCCACTCCCCCTCTACTCTCTAGAGACTGGCTGATGAAG	1803
Db	3622	CAGCCTGTGTTCCCCCACTTCCACTCCCCCTCTACTCTCTAGAGACTGGCTGATGAAG	3681
QY	1804	CACGTGCCAAATTTTCCCTTACCCCGAACTTTCCCTTACCCCGAACTTTCCCAACAGCT	1863
Db	3682	CACGTGCCAAATTTTCCCTTACCCCGAACTTTCCCTTACCCCGAACTTTCCCAACAGCT	3741
QY	1864	CCACAAACCTGTTTGGAGCTACTGACGAGACCAAGAGCACAAAAGTGCGGTTTCCCAAGCT	1923
Db	3742	CCACAAACCTGTTTGGAGCTACTGACGAGACCAAGAGCACAAAAGTGCGGTTTCCCAAGCT	3801
QY	1924	TTGTTCATCTCAGCCCCCAGAGTATCTGTGTGGGAAATCTTCAACAGAACTCAGG	1983
Db	3802	TTGTTCATCTCAGCCCCCAGAGTATCTGTGTGGGAAATCTTCAACAGAACTCAGG	3861
QY	1984	AGCAACCCCTGCTGAGCTAAGAGGAGTCTATCTCTAAGGGGGGTTAATGTCGGTTT	2043
Db	3862	AGCAACCCCTGCTGAGCTAAGAGGAGTCTATCTCTAAGGGGGGTTAATGTCGGTTT	3921
QY	2044	GCAATTAATGTGCTTATTTATTTTACGGGGTGAATATTTTAACTGTAAGTGAATC	2103
Db	3922	GCAATTAATGTGCTTATTTATTTTACGGGGTGAATATTTTAACTGTAAGTGAATC	3981
QY	2104	AGAGTAAATGTTTATGTGTGACAAATTTAAAGGCTTCTTATATGTTTA 2152	
Db	3982	AGAGTAAATGTTTATGTGTGACAAATTTAAAGGCTTCTTATATGTTTA 4030	

RESULT 14			
AR564090			
LOCUS	AR564090	4034 bp	DNA
DEFINITION	Sequence 704 from patent US 6759515.	linear	PAT 08-OCT-2004
ACCESSION	AR564090		
VERSION	AR564090.1	GI:53979141	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
1	(bases 1 to 4034)		

AUTHORS		TITLE		JOURNAL FEATURES		ORIGIN	
Xu, J., Dillon, D. C., Mitcham, R. L., Harlocker, S. L., Jiang, Y., Kalos, M. D., Fanger, G. R., Reiter, J. M., Rutter, J. A., Day, C. H., Vedivick, T. S., Carter, D., Li, S. X., Wang, A., Skeiky, Y. A. W., Hepler, W. T. and Henderson, R. A.		Compositions and methods for the therapy and diagnosis of prostate cancer		Patent: US 6759515-A 704 06-JUL-2004; location/Qualifiers 1. 4034 /organism="unknown" /mol_type="genomic DNA"			
Query	Match	91.4%	Score 1968;	DB 6;	Length 4034;		
Best Local Similarity	100.0%	Prod. No. 0;					
Matches 2088;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1;			
64	AGGCGTTTCGATGAGGAGCAGCTGAGGAGCTGTTTCCTGACAGTGCAGCATCTCCGTCTTCTC	123					
1943	AGGCGTTTCGATGAGGAGCAGCTGAGGAGCTGTTTCCTGACAGTGCAGCATCTCCGTCTTCTC	2002					
124	TCTGTCATGAGACCGGCGTGTGTCAGACCATTTGGCACTTCAGACAGTCTATTGGCCAGTGT	183					
2003	TCTGTCATGAGACCGGCGTGTGTCAGACCATTTGGCACTTCAGACAGTCTATTGGCCAGTGT	2062					
184	GACAGCTTTCCCTGAGGCTGCGCGGACCAATGCTGTCGCCACAGTGTGCGGTGTAC	243					
2063	GACAGCTTTCCCTGAGGCTGCGCGGACCAATGCTGTCGCCACAGTGTGCGGTGTAC	2122					
244	AGCTTCAGCCGCGCTCAGCCGAGTTCACTTTCAGCCCTGAGATTCCTGCCCTACACT	303					
2123	AGCTTCAGCCGCGCTCAGCCGAGTTCACTTTCAGCCCTGAGATTCCTGCCCTACACT	2182					
304	GCGCTCCCTCTTACCAACCGGAGAGAACAGATGTTCTCTGCCAATATCCAGGGGACACTGG	363					
2183	GCGCTCCCTCTTACCAACCGGAGAGAACAGATGTTCTCTGCCAATATCCAGGGGACACTGG	2242					
364	AGGTGCTAGCAGTAGAGGACAGCTGATGACACAGCTTCCTGCGCAGGCCCTTAGCTGAGAC	423					
2243	AGGTGCTAGCAGTAGAGGACAGCTGATGACACAGCTTCCTGCGCAGGCCCTTAGCTGAGAC	2302					
424	TCCCTTCCTTATAGACACAGTGGGTGTGAGGAGCAGTGGCCCTGTCCACCTCCACCCGC	483					
2303	TCCCTTCCTTATAGACACAGTGGGTGTGAGGAGCAGTGGCCCTGTCCACCTCCACCCGC	2362					
484	GCTCTGCGGGGCGCTCTGCTGTGATGTCTCCGTACGTGTGGTGGGTGAGGCCACCGA	543					
2363	GCTCTGCGGGGCGCTCTGCTGTGATGTCTCCGTACGTGTGGTGGGTGAGGCCACCGA	2422					
544	GAGCCAGGGTGTTCGCGGCGCGGGGACATCTGCTGCTGACCTGCGCAATCTCGATAGTGCCTT	603					
2423	GAGCCAGGGTGTTCGCGGCGCGGGGACATCTGCTGCTGACCTGCGCAATCTCGATAGTGCCTT	2482					
604	CTGTGCTCCAGGTGGGCGCCCATCTGTGTTATGGGCTCCATTGTCCAGCTCAGCCAGTC	663					
2483	CTGTGCTCCAGGTGGGCGCCCATCTGTGTTATGGGCTCCATTGTCCAGCTCAGCCAGTC	2542					
664	TGTACAGCCCTAATATGATGTGTGCGCGAGCGTGGGTCTGGTGGCCATTACTTTGTCTAC	723					
2543	TGTACAGCCCTAATATGATGTGTGCGCGAGCGTGGGTCTGGTGGCCATTACTTTGTCTAC	2602					
724	ACAGGTAGTATTATACAAAGACGACTTGGCCAAATATCTCAGCTGAGAAATCTTCACGAC	783					
2603	ACAGGTAGTATTATACAAAGACGACTTGGCCAAATATCTCAGCTGAGAAATCTTCACGAC	2662					
784	ATTGGAGTGAAGGAGCTGTGCTCATCTGGGTCCAGCTCCCGGCTCTCTGTAGCCCATGGG	843					
2663	ATTGGAGTGAAGGAGCTGTGCTCATCTGGGTCCAGCTCCCGGCTCTCTGTAGCCCATGGG	2722					
844	GCTGCGCGGGCGCGCGCAGTTTCTGTATGTCGCAAAATATATGAGGCTCTGTGTCGAC	903					
2723	GCTGCGCGGGCGCGCGCAGTTTCTGTATGTCGCAAAATATATGAGGCTCTGTGTCGAC	2782					

Qy	901	CCGTGCTGCTGAGTGTGCTGTAAGCTGTGCAAGCTGGGGGCTGGGGCTCCCTCTCTCTC	963
Db	2783	CTGTGTCTGTGAGTGTGCTGTAAGCTGTGCAAGCTGGGGGCTGGGGGCTCCCTCTCTCTC	284
Qy	964	CCCAAGTCTCTAGGGCTCTCTGACTGGAGGGCTTCCAGGGGGTTTCAAGTCTGGACTTATA	102
Db	2843	CCCAAGTCTCTAGGGCTCTCTGACTGGAGGGCTTCCAGGGGGTTTCAAGTCTGGACTTATA	290
Qy	1024	CAGGAGGCCAGAAAGGCTCCATGCACTGGAAATGCGGGGACTGTGCAAGTGTATCCCA	108
Db	2903	CAGGAGGCCAGAAAGGCTCCATGCACTGGAAATGCGGGGACTGTGCAAGTGTATCCCA	296
Qy	1084	GGCTCAGGGTTAAACAGCTAGCTCTCCATGTTAGACAACACTAGAGAAAGGTTTTGGAG	114
Db	2963	GGCTCAGGGTTAAACAGCTAGCTCTCCATGTTAGACAACACTAGAGAAAGGTTTTGGAG	302
Qy	1144	CTGAATTAATCACTGCACTGCTGGTTTCCCATCTCTAAGCCCCCTTAACCTGCAAGTGTGTT	120
Db	3023	CTGAATTAATCACTGCACTGCTGGTTTCCCATCTCTAAGCCCCCTTAACCTGCAAGTGTGTT	308
Qy	1204	AATGTAGCTCTTGCACTGGAGGTTTCTAAGATGAAACACTCTCATGGGATTTTGAACATA	126
Db	3083	AATGTAGCTCTTGCACTGGAGGTTTCTAAGATGAAACACTCTCATGGGATTTTGAACATA	314
Qy	1264	TGAAAGTTATTTGTAGGGGAGAGACTCTGAGGGCAACACAAGAACAGAGTCCCCCTCA	132
Db	3143	TGAAAGTTATTTGTAGGGGAGAGACTCTGAGGGCAACACAAGAACAGAGTCCCCCTCA	320
Qy	1324	GGCCACAGACCTGTCTTTTGTGTCATCCACCCCTCTTAACCTTTATACAGATGTGGCC	138
Db	3203	GGCCACAGACCTGTCTTTTGTGTCATCCACCCCTCTTAACCTTTATACAGATGTGGCC	326
Qy	1384	TGTTGTCTCTTCTGTGTGCATCAACAGACATTTAAATATTTAACCTAATTATTT	144
Db	3262	TGTTGTCTCTTCTGTGTGCATCAACAGACATTTAAATATTTAACCTAATTATTT	332
Qy	1444	TTAACAAAGTGAAGGGAATCCATTTGCTAGCTTTTCTGTGTGTCTAATAATTTGGGTA	150
Db	3322	TTAACAAAGTGAAGGGAATCCATTTGCTAGCTTTTCTGTGTGTCTAATAATTTGGGTA	338
Qy	1504	GGGTGGGGGATCCCCAACAATCAGGTCCCTGAGATGAGCGGTCATTTGGGCTGATCATTTG	156
Db	3382	GGGTGGGGGATCCCCAACAATCAGGTCCCTGAGATGAGCGGTCATTTGGGCTGATCATTTG	344
Qy	1564	CCAGAAATCTTCTTCTCTGTGGGCTCTGGCCCCCAAAATGCTTAACCCAGAACCTTGGAAA	162
Db	3442	CCAGAAATCTTCTTCTCTGTGGGCTCTGGCCCCCAAAATGCTTAACCCAGAACCTTGGAAA	350
Qy	1624	TTCTACTCATCCCAAAATGATTAATCCAAATGCGTTAATCCCAAGTTAGGGTGTGAAGA	168
Db	3502	TTCTACTCATCCCAAAATGATTAATCCAAATGCGTTAATCCCAAGTTAGGGTGTGAAGA	356
Qy	1684	AGGTAGAGGGTGGGGCTTCAGGTCTCAACGGGCTTCCCTAACACCCCTCTTCTCTTGGCC	174
Db	3562	AGGTAGAGGGTGGGGCTTCAGGTCTCAACGGGCTTCCCTAACACCCCTCTTCTCTTGGCC	362
Qy	1744	CAGCTGGGTTCCCCCACTTCCACTCCCTCTAATCTCTTGAAGACTGGGCTGATGAAG	180
Db	3622	CAGCTGGGTTCCCCCACTTCCACTCCCTCTAATCTCTTGAAGACTGGGCTGATGAAG	368
Qy	1804	CAGTCCCAAAATTTTCCCTACCCCCCACTTTCCTCAACCCCACTTTCCTCCACAGCT	186
Db	3682	CAGTCCCAAAATTTTCCCTACCCCCCACTTTCCTCAACCCCACTTTCCTCCACAGCT	374
Qy	1864	CCACAACCTGTTTGGAGTACTGCAAGAACCAAGAACCAAGTGGGTTTTCCAAAGCT	192
Db	3742	CCACAACCTGTTTGGAGTACTGCAAGAACCAAGAACCAAGTGGGTTTTCCAAAGCT	380
Qy	1924	TTGTTCATCTCAGCCCCCAGAGTATATCTGTGCTTGGGGAATCTCAACAGAAATTCAG	198
Db	3802	TTGTTCATCTCAGCCCCCAGAGTATATCTGTGCTTGGGGAATCTCAACAGAAATTCAG	386
Qy	1984	AGCAACCCCTGCTGAGCTAAGAGAGGCTTATCTCTCAGGGGGGTTTAAGTCCGTTT	204

Db	3862	AGCACCCTGCCTGAGCTAAGGAGAGCTTATCTCTCAGGGGGGTTAAAGTCCGCTT	392
Qy	2044	GCAATAATGCTCTATTATTATTCAGGGGGGATATTTTATCTGTAAGAGCAATC	2107
Db	3922	GCAATATATGCTCTATTATTATTCAGGGGGGATATTTTATCTGTAAGAGCAATC	3981
Qy	2104	AGAGTAAATGTTATGCTGACAAATTAAGGCTTCTTATATGTTA	2152
Db	3982	AGAGTAAATGTTATGCTGACAAATTAAGGCTTCTTATATGTTA	4030
RESULT 15			
LOCUS	AX200995	4034 bp	DNA linear
DEFINITION	Sequence 625 from Patent WO0151633.		
ACCESSION	AX200995		
VERSION	AX200995.1	GI:15390822	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Xu, J., Dillon, D. C., Micham, J. L., Harlocker, S. L., Jiang, Y., Reed, S. G., Kalou, M. D., Fanger, G. R., Day, C. H., Rether, M. W., Stock, J. A., Skeiky, Y. A., Wang, A. and Mesgher, M. J.		
TITLE	Compositions and methods for the therapy and diagnosis of prostate cancer		
JOURNAL	Patent: WO 0151633-A 625 19-JUL-2001;		
FEATURES	CORPORA CORPORATION (US)		
source	Location/Qualifiers		
	1..4034		
	/organism="Homo sapiens"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
ORIGIN			
Query Match	91.4%; Score 1968; DB 6; Length 4034;		
Best Local Similarity	100.0%; Pred. No. 0;		
Matches 2088; Conservative	0; Mismatches	0; Indels	1; Gaps
Qy	64	AGGCGTTGGATGGGACGCTTGAGGCGTGTTCCTGACGTGCGCCATCTCCTGCTTCTC	123
Db	1943	AGGCGTTGGATGGGACGCTTGAGGCGTGTTCCTGACGTGCGCCATCTCCTGCTTCTC	2002
Qy	124	TCTGGTCAATGACCGGCTGTGACGCGATTCGACATTCGACAGCTTATTTGGCGAGTGT	183
Db	2003	TCTGGTCAATGACCGGCTGTGACGCGATTCGACATTCGACAGCTTATTTGGCGAGTGT	2062
Qy	184	GAGCAGCTTTCCTGTGCTGCGGCTGCGACATGCTCTTCCACAGTGTGGCGTGTGAC	243
Db	2063	GAGCAGCTTTCCTGTGCTGCGGCTGCGACATGCTCTTCCACAGTGTGGCGTGTGAC	2122
Qy	244	AGCTTCAGCGCCCTTCACCGGCTTCACTTCTCAGCCCTGAGATCTCTGCCCTTACACT	303
Db	2123	AGCTTCAGCGCCCTTCACCGGCTTCACTTCTCAGCCCTGAGATCTCTGCCCTTACACT	2182
Qy	304	GAGCTTCCTTCACACCGGAGAGACAGGTGTTCTGSCCAATATACGAGGGGACATGG	363
Db	2183	GAGCTTCCTTCACACCGGAGAGACAGGTGTTCTGSCCAATATACGAGGGGACATGG	2242
Qy	364	AGGTGCTAAGCAGTGAAGACAGCTGATGACCAAGCTTCTGSCCAAGCCCTTAAGCTGAGC	423
Db	2243	AGGTGCTAAGCAGTGAAGACAGCTGATGACCAAGCTTCTGSCCAAGCCCTTAAGCTGAGC	2302
Qy	424	TTCCTTCCTTAATGACACAGTGGGTGCTGAGGACAGTGGGCTCTCCCACTCAACCCGC	483
Db	2303	TTCCTTCCTTAATGACACAGTGGGTGCTGAGGACAGTGGGCTCTCCCACTCAACCCGC	2362
Qy	484	GCTTCGCGGGGCTCTGCTGTGATGTCTCCATAGTGTGTGTGTGAGCCACCGA	543
Db	2363	GCTTCGCGGGGCTCTGCTGTGATGTCTCCATAGTGTGTGTGTGAGCCACCGA	2422

QY 544 GGCAGGGGATTCGGGGCCGGGGCATCTGCGTGAACCTCGCCATCTGGATAGTGCCTT 603
 DB 2423 GGCAGGGGATTCGGGGCCGGGGCATCTGCGTGAACCTCGCCATCTGGATAGTGCCTT 2482
 QY 604 CCTGCTGTCCAGTGTGGCCCATCTCTGTTATGAGCTCCATTGTCAGCTCAGCCAGTC 663
 DB 2483 CCTGCTGTCCAGTGTGGCCCATCTCTGTTATGAGCTCCATTGTCAGCTCAGCCAGTC 2542
 QY 664 TGTCACTGCTATATGTGTCTGCGCAGAGCTGGGTCTGTGTGCCATTAACTTTGCTAC 723
 DB 2543 TGTCACTGCTATATGTGTCTGCGCAGAGCTGGGTCTGTGTGCCATTAACTTTGCTAC 2602
 QY 724 ACAGGATGATTGACAGAGGCACTTGGCCAAATCTAGAGGTAAATACTTCCAGAC 783
 DB 2603 ACAGGATGATTGACAGAGGCACTTGGCCAAATCTAGAGGTAAATACTTCCAGAC 2662
 QY 784 ATTTGGGATGAGGAGCTGCTCACTGGATCCAGCTCCCGCTCTGTTAGCCCAATGG 843
 DB 2663 ATTTGGGATGAGGAGCTGCTCACTGGATCCAGCTCCCGCTCTGTTAGCCCAATGG 2722
 QY 844 GCTGCCGGGCTGGCCGCAAGTTCTGTGTCTGCAAAATATGTGCTCTGTGCGAC 903
 DB 2723 GCTGCCGGGCTGGCCGCAAGTTCTGTGTCTGCAAAATATGTGCTCTGTGCGAC 2782
 QY 904 CCTGTGCTGTAGAGTGGTGAAGCTGACAGCTGGGGGGCTGGGGCCCTCTCTCTCTC 963
 DB 2783 CCTGTGCTGTAGAGTGGTGAAGCTGACAGCTGGGGGGCTGGGGCCCTCTCTCTCTC 2842
 QY 964 CCCAGCTCTAGAGGCTGCTGACTGAGAGGCTTCCAAAGGGGTTTCACTGGAATTATA 1023
 DB 2843 CCCAGCTCTAGAGGCTGCTGACTGAGAGGCTTCCAAAGGGGTTTCACTGGAATTATA 2902
 QY 1024 CAGGGAGGCCAAGAGGGCTTCATGCACTGGAATGCGGGACCTTCGAGGTGATTAACCA 1083
 DB 2903 CAGGGAGGCCAAGAGGGCTTCATGCACTGGAATGCGGGACCTTCGAGGTGATTAACCA 2962
 QY 1084 GGCTCAGGGTTAAACGCTAGCCCTCCCTAGTTGAGACACACTCTAGAGAAAGGTTTGGAG 1143
 DB 2963 GGCTCAGGGTTAAACGCTAGCCCTCCCTAGTTGAGACACACTCTAGAGAAAGGTTTGGAG 3022
 QY 1144 CTGAATTAACCTAGTCACTGCTGTTTCCATCTCTAAGCCCTTAACTGACGCTTGTT 1203
 DB 3023 CTGAATTAACCTAGTCACTGCTGTTTCCATCTCTAAGCCCTTAACTGACGCTTGTT 3082
 QY 1204 AATGTAGCTCTTGATGAGGATTTCTAGAGTAAACATCTTCATGAGGATTTGAACATA 1263
 DB 3083 AATGTAGCTCTTGATGAGGATTTCTAGAGTAAACATCTTCATGAGGATTTGAACATA 3142
 QY 1264 TGAAGTTATTTGTAGGGGAAAGTCTGAGGGGCAACACAGAAACAGAGTCCCTCA 1323
 DB 3143 TGAAGTTATTTGTAGGGGAAAGTCTGAGGGGCAACACAGAAACAGAGTCCCTCA 3202
 QY 1324 GCCCAGAGCACTGCTTTTGTGATCAACCCCTCTTACCTTTATCAGAGTGTGGCC 1383
 DB 3203 GCCCAGAGCACTGCTTTTGTGATCAACCCCTCTTACCTTTATCAGAGTGTGGCC 3261
 QY 1384 TGTGTGCTCTTCTGTTGCCATCACAGACACAGGCAATTAAATATTATTTATTT 1443
 DB 3263 TGTGTGCTCTTCTGTTGCCATCACAGACACAGGCAATTAAATATTATTTATTTATTT 3321
 QY 1444 TTAACAAAGTAAAGGAATCCATGTGCTAGCTTTCTGTGTGTGCTAATATTGGGTA 1503
 DB 3322 TTAACAAAGTAAAGGAATCCATGTGCTAGCTTTCTGTGTGTGCTAATATTGGGTA 3381
 QY 1504 GGTGGGGGATCCCAACATAGGTCCTGAGATAGCTGTGATTTGGGCTGATCATTTG 1563
 DB 3382 GGTGGGGGATCCCAACATAGGTCCTGAGATAGCTGTGATTTGGGCTGATCATTTG 3441
 QY 1564 CCAGAACTCTTCTCTGCGGGCTGTGGCCCTCCCAAAATGCTTAACCCAGAGCTTTGAAA 1623
 DB 3442 CCAGAACTCTTCTCTGCGGGCTGTGGCCCTCCCAAAATGCTTAACCCAGAGCTTTGAAA 3501

QY 1624 TTCTACTATCCCAATGATTAATTCAAATGCTGTACCAAGGTTAGGGTGTGAAGA 1683
 DB 3502 TTCTACTATCCCAATGATTAATTCAAATGCTGTGTACCAAGGTTAGGGTGTGAAGA 3561
 QY 1684 AGGTAGAGGGTGGGCTTCAGGCTTCACAGGCTTCCCTAACCAACCCCTCTCTTGTGAC 1743
 DB 3562 AGGTAGAGGGTGGGCTTCAGGCTTCACAGGCTTCCCTAACCAACCCCTCTCTTGTGAC 3621
 QY 1744 CAGCTGTGTCCCCCACTTCCATCTCCCTTACTCTCTGTAGACTGGGCTGATGAAG 1803
 DB 3622 CAGCTGTGTGTCCCCCACTTCCATCTCCCTTACTCTCTGTAGACTGGGCTGATGAAG 3681
 QY 1804 CACTGCCAAATTTCCCTTACCCCACTTCCCTTACCCCACTTCCCAACAGCT 1863
 DB 3682 CACTGCCAAATTTCCCTTACCCCACTTCCCTTACCCCACTTCCCAACAGCT 3741
 QY 1864 CCACAACTCTGTTGAGCTACTGACAGACAGAAACAAAGTGGGTTTCCAGGCT 1923
 DB 3742 CCACAACTCTGTTGAGCTACTGACAGACAGAAACAAAGTGGGTTTCCAGGCT 3801
 QY 1924 TTGTCCATCTAGCCCCCAGAGTATCTGTGCTTGGGGAATCTCACACAGAACTCAG 1983
 DB 3802 TTGTCCATCTAGCCCCCAGAGTATCTGTGCTTGGGGAATCTCACACAGAACTCAG 3861
 QY 1984 AGCAGCCCTGCTGAGCTAAGGAGGCTTATCTCTCAAGGGGGGTTAAGTCCGCTT 2043
 DB 3862 AGCAGCCCTGCTGAGCTAAGGAGGCTTATCTCTCAAGGGGGGTTAAGTCCGCTT 3921
 QY 2044 GCAATTAATGCTCTTATTTATTTAGCGGGGTAATTTTAACTGTAACTGACAAATC 2103
 DB 3922 GCAATTAATGCTCTTATTTATTTAGCGGGGTAATTTTAACTGTAACTGACAAATC 3981
 QY 2104 AAGATTAATGTTTATGTGACAAATTAAGGCTTTCTTATATGTTTA 2152
 DB 3982 AAGATTAATGTTTATGTGACAAATTAAGGCTTTCTTATATGTTTA 4030

Search completed: February 8, 2005, 17:33:41
 Job time : 9273.38 secs

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 8, 2005, 11:26:32 ; Search time 7011.66 Seconds
(without alignments)
11682.581 Million cell updates/sec

Title: US-09-841-894a-16

Perfect score: 2152
Sequence: 1 GGGGCTGACCAAGCGCGTCG.....AAGCTTCTATATGTTA 2152

Scoring table: OLIGO-MVC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_g881:*
9: gb_g882:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2088	97.0	2477	3	HSMB04244
2	722	33.6	722	7	CN373215
3	704	32.7	1626	9	AY407706
4	659	30.6	1025	5	BM915082
5	656	30.5	897	6	CA489628
6	644	29.9	670	5	BU689021
7	638	29.6	651	6	CB048223
8	617	28.7	916	5	BQ950912
9	564	26.2	959	5	BQ950805
10	541	25.1	718	2	BE867241
11	528	24.5	581	7	CN373214
12	491	22.8	589	4	BG469586
13	475	22.1	875	5	BQ942028
14	474	22.0	1060	5	BM914562
15	470	21.8	515	5	BX098291
16	437	20.3	734	6	CD634718
17	430	20.0	437	7	CF135166
18	390	18.1	418	2	BF922235
19	390	18.1	599	6	CB050165
20	386	17.9	740	6	CD634716
21	382	17.8	1667	7	BM912193
22	377	17.5	494	7	CF134970
23	373	17.3	850	4	BF972601
24	353	16.4	370	2	AM135465

C 25	350	16.3	491	1	AA631143
C 26	347	16.1	412	2	AM175665
C 27	332	15.4	469	1	AT103348
C 28	331	15.4	410	6	CD634731
C 29	331	15.4	413	6	CD634732
C 30	331	15.4	756	6	CD634730
C 31	321	14.9	325	2	BE673709
C 32	319	14.8	327	1	AT169820
C 33	319	14.8	448	2	BE674096
C 34	316	14.7	435	6	CB049513
C 35	315	14.6	320	2	BF222329
C 36	314	14.6	315	1	AA640153
C 37	312	14.5	320	2	BF223843
C 38	311	14.5	313	1	AT187483
C 39	306	14.2	306	1	AA631024
C 40	303	14.1	388	1	AA579486
C 41	300	13.9	800	4	BG469487
C 42	300	13.9	894	4	BG469520
C 43	295	13.7	949	4	BG255296
C 44	293	13.6	313	6	CB050330
C 45	283	13.2	737	6	CD634720

ALIGNMENTS

RESULT 1
LOCUS HSM804244
DEFINITION Homo sapiens mRNA; cDNA DKFP666D0110 (from clone DKFP666D0110).
ACCESSION AL832933
VERSION AL832933.1 GI:21733520
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 2477)
Ansoorge, W., Krieger, S., Regiert, T., Rittmuller, C., Schwager, B., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.
The German cDNA Consortium
Direct Submission
Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratory), Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.
This clone (DKFP666D0110) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFP666D0110
Further information about the clone and the sequencing project is available at <http://mips.gsf.de/projects/cdna/>.
location/Qualifiers
1. 2477
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="RZPD:DKFP666D0110"
/db_xref="taxon:9606"
/clone="DKFP666D0110"
/clone_lib="666 (synonym: h602). Vector pSport1; host DH10B; sites NotI + SalI"
/dev_stage="adult"
/note="proteins, alternative start, differentially spliced"
1. 2477
/gene="DKFP666D0110"
370. 1065
/gene="DKFP666D0110"

```
/codon_start=1
/product="hypothetical protein"
/protein_id="CAH56282.1"
/db_xref="GI:52545721"
/translation="MSGSLGFLQCAISLVESLVWMLVORFGRAYLVASVAPVAA
GATLSHVAVTWASALYGFPSALDILPYTLASLYHREKQVFLRYKNDGASSE
DSMTSFLPGPKPAPNGHVGAGSSGILPPPALCGASACVSRVYVGEETEARV
VPRGICLDLAIIDSAFLISQVAPSLFMSIVQLSOSVTAIVMSAAGLVAIFPATQ
VFPDKSLAKRYSA"
```

```
Query Match      97.0%; Score 2088; DB 3; Length 2477;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2088; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 GGCCTTGGATGGGACGCTGGGGCTGTTCTTCGAGTGGCCATCTCCGATCTTCTCT 124
DB 361 GGGCTTGGATGGGACGCTGGGGCTGTTCTTCGAGTGGCCATCTCCGATCTTCTCT 420
QY 125 CTGGTCATGGACCGGGCTGGTGCAGCAATGGGCACTGGACATCTTATTTGGCACTGG 184
DB 421 CTGGTCATGGACCGGGCTGGTGCAGCAATGGGCACTGGACATCTTATTTGGCACTGG 480
QY 185 GCAGCTTTCCTGTGGCTGGCGGTGCCACATGCTGTCCCAAGTGTGGCGGTGGTACA 244
DB 481 GCAGCTTTCCTGTGGCTGGCGGTGCCACATGCTGTCCCAAGTGTGGCGGTGGTACA 540
QY 245 GCTTCAGCGCGCTTCACCGGGTTCACCTTTCAGCCCTGAGATCTGCGCTTACACATG 304
DB 541 GCTTCAGCGCGCTTCACCGGGTTCACCTTTCAGCCCTGAGATCTGCGCTTACACATG 600
QY 305 GCTTCCTCTTACCAACCGGGAGAGACAGTGTCTCTGCCCAATATCCGAGGGGCACTGGA 364
DB 601 GCTTCCTCTTACCAACCGGGAGAGACAGTGTCTCTGCCCAATATCCGAGGGGCACTGGA 660
QY 365 GGTGTCTAGCAGTGAAGACAGCTGATGACCAAGTTCTTCGACAGCCCTTAAGCCTGAGCT 424
DB 661 GGTGTCTAGCAGTGAAGACAGCTGATGACCAAGTTCTTCGACAGCCCTTAAGCCTGAGCT 720
QY 425 CCCTTCCCTTAATGAGACAGTGGGTGCTGAGAGGAGAGGCTGCTGCCAATCTTCAACCGCG 484
DB 721 CCCTTCCCTTAATGAGACAGTGGGTGCTGAGAGGAGAGGCTGCTGCCAATCTTCAACCGCG 780
QY 485 CTCTGCGGGGCTCTCTGCTGTGATGTCTCCGATAGTGTGTGTGTGTGTGTGTGTGTGTGT 544
DB 781 CTCTGCGGGGCTCTCTGCTGTGATGTCTCCGATAGTGTGTGTGTGTGTGTGTGTGTGTGT 840
QY 545 GCCAGGGTGTGTCCGGGCGGGGCGGACATCTGCTGACCTTGGCATCTGTGATGTGTCTTC 604
DB 841 GCCAGGGTGTGTCCGGGCGGGGCGGACATCTGCTGACCTTGGCATCTGTGATGTGTCTTC 900
QY 605 CTGCTGTCCAGAGTGGCCCATCTCCGTTATGGGCTCCATGTTGCAAGTCCAGAGCT 664
DB 901 CTGCTGTCCAGAGTGGCCCATCTCCGTTATGGGCTCCATGTTGCAAGTCCAGAGCT 960
QY 665 GTCACTGCTTAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 724
DB 961 GTCACTGCTTAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
QY 725 CAGGTATGTTTGAACAAGGCGACTTGGCCAAATCTCAGGCTAATAAACTTCCAGCA 784
DB 1021 CAGGTATGTTTGAACAAGGCGACTTGGCCAAATCTCAGGCTAATAAACTTCCAGCA 1080
QY 785 TTGGGGGTGAGGGCTGCTCACTGGGTCCAGCTCCCGCTCTGTTAGCCCACTGGGG 844
DB 1081 TTGGGGGTGAGGGCTGCTCACTGGGTCCAGCTCCCGCTCTGTTAGCCCACTGGGG 1140
QY 845 CTGCGCGGGCTGGCGCCGCAAGTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 904
DB 1141 CTGCGCGGGCTGGCGCCGCAAGTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1200
QY 905 CTGTCTCTGAGTGTGCGTATGCAAGCTGGGGGGCTGGGGCGTCCCTCTCTCTCC 964
```

```
DB 1201 CTGTGCTGTGAGTGTGCGTATGCAAGCTGGGGGCTGGGGCGTCCCTCTCTCTCTCC 1260
QY 965 CCAGTCTCTAGGGGCTGCCCTGACCTGGAGGCGCTTCCAGGGGGGTTTACGTCTGACCTTATAC 1024
DB 1261 CCAGTCTCTAGGGGCTGCCCTGACCTGGAGGCGCTTCCAGGGGGGTTTACGTCTGACCTTATAC 1320
QY 1025 AAGGAGGCCGAGAGGGCTTCATGCACTGAAATGCGGGGACTCTGCAAGGTGATTAACCGAG 1084
DB 1321 AAGGAGGCCGAGAGGGCTTCATGCACTGAAATGCGGGGACTCTGCAAGGTGATTAACCGAG 1380
QY 1085 GCTCAGGGGTAAACAGCTAGCCCTCCATGTTGAGACACACTTATAGAGAGGGTTTTGGAGC 1144
DB 1381 GCTCAGGGGTAAACAGCTAGCCCTCCATGTTGAGACACACTTATAGAGAGGGTTTTGGAGC 1440
QY 1145 TGAATTAATCTCAGTCACTGGTTTCCCATCTCTAAGCCCTTAACCTGACGCTTGTTA 1204
DB 1441 TGAATTAATCTCAGTCACTGGTTTCCCATCTCTAAGCCCTTAACCTGACGCTTGTTA 1500
QY 1205 ATGTAGCTCTTGCATGGAGGATTTCTAGAGTAAACACTCTCTCATGGGATTTGAACATAT 1264
DB 1501 ATGTAGCTCTTGCATGGAGGATTTCTAGAGTAAACACTCTCTCATGGGATTTGAACATAT 1560
QY 1265 GAAAGTTATTTGTAGGGGAGAGTCTGAGGGGCAACACAAAGAACAGATCCCTCAG 1324
DB 1561 GAAAGTTATTTGTAGGGGAGAGTCTGAGGGGCAACACAAAGAACAGATCCCTCAG 1620
QY 1325 CCACAGCAGCTGTCTTTTGTGTGATCCACCCCTCTTACCTTTATCAGAGATGGCCT 1384
DB 1621 CCACAGCAGCTGTCTTTTGTGTGATCCACCCCTCTTACCTTTATCAGAGATGGCCT 1680
QY 1385 GTTGTGCTCTGTGTGCTATCAGACAGACACAGCATTTAATTTTAACTTATTTT 1444
DB 1681 GTTGTGCTCTGTGTGCTATCAGACAGACACAGCATTTAATTTTAACTTATTTT 1740
QY 1445 AACAAAGTAAAGGAGAAATCCATGTCTAGCTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1504
DB 1741 AACAAAGTAAAGGAGAAATCCATGTCTAGCTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1800
QY 1505 GGTGGGGGATCCCAACATCAGGTCCTCTGAGATGCTGTGCTATTTGGGCTGATCATTTGC 1564
DB 1801 GGTGGGGGATCCCAACATCAGGTCCTCTGAGATGCTGTGCTATTTGGGCTGATCATTTGC 1860
QY 1565 CAGATCTTCTTCTCCGCGGGGTGCGCCGCCCAAAAGCCCTTAACCCGAGACCTTGGAAAT 1624
DB 1861 CAGATCTTCTTCTCCGCGGGGTGCGCCGCCCAAAAGCCCTTAACCCGAGACCTTGGAAAT 1920
QY 1625 TCTACTCATCCCAATGATTAATTCCTGTTACCTCAAGGTTAGGGTGTGAAGAA 1684
DB 1921 TCTACTCATCCCAATGATTAATTCCTGTTACCTCAAGGTTAGGGTGTGAAGAA 1980
QY 1685 GGTAGAGGTGGGGCTTCAGGTCTCAACGGCTTCCCTAACCAACCCTCTTCTGTGGCCC 1744
DB 1981 GGTAGAGGTGGGGCTTCAGGTCTCAACGGCTTCCCTAACCAACCCTCTTCTGTGGCCC 2040
QY 1745 AGCTGTGTTCCCCCACTTCCATCTCCCTCTACTCTCTAAGAGCTGGGCTGATGAAGGC 1804
DB 2041 AGCTGTGTTCCCCCACTTCCATCTCCCTCTACTCTCTAAGAGCTGGGCTGATGAAGGC 2100
QY 1805 ACTGCCCAAAATTTCCCTTACCCCACTTCCCTTACCCCACTTCCCAAGCTC 1864
DB 2101 ACTGCCCAAAATTTCCCTTACCCCACTTCCCTTACCCCACTTCCCAAGCTC 2160
QY 1865 CACAACCTGTGTGAGAGCTATCTGCAAGACCAAGAACCAAAAGTGGGTTTTCCAGGCTT 1924
DB 2161 CACAACCTGTGTGAGAGCTATCTGCAAGACCAAGAACCAAAAGTGGGTTTTCCAGGCTT 2220
QY 1925 TGTCAATCTCAGCCCCAGAGTATATCTGTGTTGGGGAATCTCACAGAAACTCAGGA 1984
DB 2221 TGTCAATCTCAGCCCCAGAGTATATCTGTGTTGGGGAATCTCACAGAAACTCAGGA 2280
QY 1985 GCAACCCCTGCTGAGCTAAAGGAGGTTTATCTCTCAGGGGGGGTTTAAAGTCCGTTTG 2044
DB 2281 GCAACCCCTGCTGAGCTAAAGGAGGTTTATCTCTCAGGGGGGGTTTAAAGTCCGTTTG 2340
```

QY 2045 CATAATGCTCTTATTATTATTTAGCGGGGTGAATTTTATCTGTAAGTGCATCA 2104
DB 2341 CATAATGCTCTTATTATTATTTAGCGGGGTGAATTTTATCTGTAAGTGCATCA 2400
QY 2105 GAGTATATGTTATGATGACAAATAATTAAGGCTTCTTATATGTTTA 2152
DB 2401 GAGTATATGTTATGATGACAAATAATTAAGGCTTCTTATATGTTTA 2448

RESULT 2
CN373215 722 bp mRNA linear EST 16-MAY-2004
LOCUS 17000532237472 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN373215
ACCESSION CN373215.1 GI:47373149
VERSION
KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Pang, R., Guejler, K., Rao, M.S., Mandalam, R.,
Lebkowicz, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert length: 722 Std Error: 0.00.
Location/Qualifiers

FEATURES
source
1..722
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cissue_type="embryonic stem cells, cell lines H1, H7, and H9"
/clone_1ib="GRN_ES"
/note="Oligo dt primed, full-length enriched cDNA library from undifferentiated hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions"

ORIGIN
Query Match 33.6%; Score 722; DB 7; Length 722;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 722; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 759 ACTGACGCGTGAAGAACTTCACAGACATTTGGGGTGAAGGGCTGCTCAGTCGGTCCAGC 818
DB 1 ACTGACGCGTGAAGAACTTCACAGACATTTGGGGTGAAGGGCTGCTCAGTCGGTCCAGC 60
QY 819 TCCCGGCTCTGTTAGCCCCCAGTGGGCTGCGGGCTGCGCCAGTTTCTGTTGTCGCA 878
DB 61 TCCCGGCTCTGTTAGCCCCCAGTGGGCTGCGGGCTGCGCCAGTTTCTGTTGTCGCA 120
QY 879 AAGTATATGCGCTCTGCTGCGCAACCTGTGCTGAGGTGCTGACGTGCACAGTGGG 938
DB 121 AAGTATATGCGCTCTGCTGCGCAACCTGTGCTGAGGTGCTGACGTGCACAGTGGG 180
QY 939 GCGTGGGGGCTCCCTCTCTCTCCCAAGTCTCTAGGGGTGCTGACTGAGAGCCCTTC 998
DB 181 GCGTGGGGGCTCCCTCTCTCTCCCAAGTCTCTAGGGGTGCTGACTGAGAGCCCTTC 240
QY 999 AAGGGGGTTTCAGTCTGACCTTATACAGGAGGCGAAAGGGCTCCATGCACTGAATGC 1058
DB 241 AAGGGGGTTTCAGTCTGACCTTATACAGGAGGCGAAAGGGCTCCATGCACTGAATGC 300

QY 1059 GGGGACTCTGACGTGATTAACCGAGGCTCAGGGTTAAAGCTAGCTTGTGAGC 1118
DB 301 GGGGACTCTGACGTGATTAACCGAGGCTCAGGGTTAAAGCTAGCTTGTGAGC 360
QY 1119 ACACCTAGAGAGGGTTTTGGAGCTGAATAACTCACTCACTGTTTCCATCTTA 1178
DB 361 ACACCTAGAGAGGGTTTTGGAGCTGAATAACTCACTCACTGTTTCCATCTTA 420
QY 1179 AGCCCTTAACCTGACGCTTCTTTATGATGACCTCTTGACAGGAGTTTCTAGATGAA 1238
DB 421 AGCCCTTAACCTGACGCTTCTTTATGATGACCTCTTGACAGGAGTTTCTAGATGAA 480
QY 1239 CACTCTTCATGAGGATTTGAAGATATGAAGTATTTGATAGGGAAGCTCTGAGGGGC 1298
DB 481 CACTCTTCATGAGGATTTGAAGATATGAAGTATTTGATAGGGAAGCTCTGAGGGGC 540
QY 1299 AACACAGAGAACGAGTCCCTCAGCCACAGCACTGCTTTTGGTCTGATCCACCCCC 1358
DB 541 AACACAGAGAACGAGTCCCTCAGCCACAGCACTGCTTTTGGTCTGATCCACCCCC 600
QY 1359 TCTTACCTTTATACAGATGAGGCTGTTGCTTCTGTTGCCATCAGAGACACAG 1418
DB 601 TCTTACCTTTATACAGATGAGGCTGTTGCTTCTGTTGCCATCAGAGACACAG 660
QY 1419 CATTAAATATTTACTTATTATTAAAGATGAAGGAATCATGCTAGCTTTC 1478
DB 661 CATTAAATATTTACTTATTATTAAAGATGAAGGAATCATGCTAGCTTTC 720
QY 1479 TG 1480
DB 721 TG 722

RESULT 3
AY407706 1626 bp DNA linear GSS 12-DEC-2003
LOCUS Homo sapiens HCM2980 gene, VIRUTAL TRANSCRIPT, partial sequence.
DEFINITION genomic survey sequence.
ACCESSION AY407706
VERSION AY407706.1 GI:39763677
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejaritwal, A.,
Todd, M.A., Tanenbaum, D.M., Civeleo, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sinsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
JOURNAL PUBMED 14671302
REFERENCE 2 (bases 1 to 1626)
AUTHORS Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejaritwal, A.,
Todd, M.A., Tanenbaum, D.M., Civeleo, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sinsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
1..1626
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>1626
/locus_tag="HCM2980"

Query Match 32.7%; Score 704; DB 9; Length 1626;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 704; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 GCGTTGGATGAGGAGCGCTGGGCTGTTCTGCGAGTGGCCATCTCCCTGGTCTTCTC 125
DB 923 GCGTTGGATGAGGAGCGCTGGGCTGTTCTGCGAGTGGCCATCTCCCTGGTCTTCTC 982
QY 126 TGGTCATGAGACCGGCTGGTGAAGAGATTCGGCACTCCAGAGCTTATTTGGCCAGTGG 185
DB 983 TGGTCATGAGACCGGCTGGTGAAGAGATTCGGCACTCCAGAGCTTATTTGGCCAGTGG 1042
QY 186 CAGCTTTCCCTGTGAGCTGCGCGGTCACATGCTGTCACAGAGTGGCGCGTGGTGAAG 245
DB 1043 CAGCTTTCCCTGTGAGCTGCGCGGTCACATGCTGTCACAGAGTGGCGCGTGGTGAAG 1102
QY 246 CTTTACGCGCGCTTACCGGGGTTTCACTTCTGACGCTTGAAGTCTTGGCCCTTACACATGG 305
DB 1103 CTTTACGCGCGCTTACCGGGGTTTCACTTCTGACGCTTGAAGTCTTGGCCCTTACACATGG 1162
QY 306 CCTCCCTCTACACACCGGAGAGAGAGGTTTCCCGCCAAATACCGAGGGGAGACATGGAG 365
DB 1163 CCTCCCTCTACACACCGGAGAGAGAGGTTTCCCGCCAAATACCGAGGGGAGACATGGAG 1222
QY 366 GTGCTAGCAGTGAAGACAGCTTGAATGACAGCTTCTGCGAGGCGCTTAAAGCTGAGCTC 425
DB 1223 GTGCTAGCAGTGAAGACAGCTTGAATGACAGCTTCTGCGAGGCGCTTAAAGCTGAGCTC 1282
QY 426 CCTCCCTCTACACACCGGAGAGAGAGGTTTCCCGCCAAATACCGAGGGGAGACATGGAG 485
DB 1283 CCTCCCTCTACACACCGGAGAGAGAGGTTTCCCGCCAAATACCGAGGGGAGACATGGAG 1342
QY 486 TCTGCGGAGGCTTGTGCTGTGATGTCTCCGTAAGTGTGTGTGTGAGCCAGCGAG 545
DB 1343 TCTGCGGAGGCTTGTGCTGTGATGTCTCCGTAAGTGTGTGTGTGAGCCAGCGAG 1402
QY 546 CCAAGGAGGTTTCCGGGCGGGGAGATCTGCTGAGACCTCCGCACTCTGATAGTGGCTTCC 605
DB 1403 CCAAGGAGGTTTCCGGGCGGGGAGATCTGCTGAGACCTCCGCACTCTGATAGTGGCTTCC 1462
QY 606 TGTGTGTCAGAGTGGGCGGATCCCTGTATTATGGGCTCCATTGTCAGCTCAGCGAGTGG 665
DB 1463 TGTGTGTCAGAGTGGGCGGATCCCTGTATTATGGGCTCCATTGTCAGCTCAGCGAGTGG 1522
QY 666 TCACTGCTTATATGATGTGTGCTGCGCAGGCGCTGGGTCTGATTTTCTTGTCTACAC 725
DB 1523 TCACTGCTTATATGATGTGTGCTGCGCAGGCGCTGGGTCTGATTTTCTTGTCTACAC 1582
QY 726 AGGTAGTATTTGACAGAGCGACTTGGCCAAATATCTCAGCGTAG 769
DB 1583 AGGTAGTATTTGACAGAGCGACTTGGCCAAATATCTCAGCGTAG 1626

RESULT 4
BM915082 1025 bp mRNA linear EST 12-MAR-2002
LOCUS AGENCOURT 6702317 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5481218
DEFINITION 5' mRNA Sequence.
ACCESSION BM915082
VERSION BM915082.1 GI:19365461
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1025)
NID-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L102005 row: 6 column: 03
High quality sequence start: 35
High quality sequence stop: 657.
Location/Qualifiers
1..1025
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5481218"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH MGC 41"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 30.6%; Score 659; DB 5; Length 1025;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 759; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 623 CCATCCCGTTTATGGGCTCATTTGTCAGTCCAGCCAGTGTGCTCATCTGCTATATGTTG 682
DB 12 CCATCCCGTTTATGGGCTCATTTGTCAGTCCAGCCAGTGTGCTCATCTGCTATATGTTG 71
QY 683 TCTGCGGAGGCTGTGGTGTGTGTGCGCATTTACTTGTCTACAGAGTAGATTGACAG 742
DB 72 TCTGCGGAGGCTGTGGTGTGTGTGCGCATTTACTTGTCTACAGAGTAGATTGACAG 131
QY 743 AGGCACTTGGCCAAATCTAGCGCTAGAAAATTCCAGACATTTGGGGTGGAGGCTGCG 802
DB 132 AGGCACTTGGCCAAATCTAGCGCTAGAAAATTCCAGACATTTGGGGTGGAGGCTGCG 191
QY 803 CTCACCTGGTCCAGGCTCCCGGCTCTGTTAGGCCCAATGGGGCTGGCGGCTGGCCCA 862
DB 192 CTCACCTGGTCCAGGCTCCCGGCTCTGTTAGGCCCAATGGGGCTGGCGGCTGGCCCA 251
QY 863 GTTTCGTGTGTCGCAAGATATGTGTGCTCTGCTGCAACCTGTGCTCTGAGTGGCG 922
DB 252 GTTTCGTGTGTCGCAAGATATGTGTGCTCTGCTGCAACCTGTGCTCTGAGTGGCG 311
QY 923 TAGCTGACAGCTGGGGGCTGGGGGCGTCCCTCTCTCTCCCAAGCTCTTAAAGGCTGCC 982
DB 312 TAGCTGACAGCTGGGGGCTGGGGGCGTCCCTCTCTCTCCCAAGCTCTTAAAGGCTGCC 371
QY 983 TGACTGAGGCTTCCAGAGGGGTTTCACTGTGACTTATACAGGAGGCCAGAGGACT 1042
DB 372 TGACTGAGGCTTCCAGAGGGGTTTCACTGTGACTTATACAGGAGGCCAGAGGACT 431
QY 1043 CCATGCACTGGGATTTGGGGGACTCTGCAAGTGTGATTACCAAGGCTCAGGGTTAAACGCTA 1102
DB 432 CCATGCACTGGGATTTGGGGGACTCTGCAAGTGTGATTACCAAGGCTCAGGGTTAAACGCTA 491
QY 1103 GCGTCTAGTTGAGACACACTTGAAGAGGTTTGGAGGCTGAAATTAATCAGTCACAC 1162
DB 492 GCGTCTAGTTGAGACACACTTGAAGAGGTTTGGAGGCTGAAATTAATCAGTCACAC 551
QY 1163 TGGTTTCCATCTTAAAGCCCTTAACTGCAAGCTTGTATATGATGCTTGTGACATGG 1222
DB 552 TGGTTTCCATCTTAAAGCCCTTAACTGCAAGCTTGTATATGATGCTTGTGACATGG 611
QY 1223 AGTTTCAAGATGAACACTCTCTCATGGGATTTGAACATTAAGAAATTATTTGATGGG 1282

Db 612 AGTTCTAGATGAACACTCTCCATGGGATTTGAACATGAAATTATTGTAGGGG 671

QY 1283 MAGAGCTCTGAGGGGCAACACACAGACAGAGTCCCTTCAGCCCAAGACATCTGTTT 1342

Db 672 MAGAGCTCTGAGGGGCAACACACAGACAGAGTCCCTTCAGCCCAAGACATCTGTTT 731

QY 1343 TGTGATCCAGCCCTCTTACCTTTATTCAGAGATGGGC 1383

Db 732 TGTGATCCAGCCCTCTTACCTTTATTCAGAGATGGGC 772

RESULT 5
CA489628
LOCUS CA489628
DEFINITION AGNCOURT_10810630 MAPCL Homo sapiens cDNA clone IMAGE:6722106 5', mRNA sequence.
ACCESSION CA489628
VERSION CA489628.1 GI:24952419
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: Kristi A. Eglund, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLM14284 row: e column: 18
High quality sequence stop: 625.
Location/Qualifiers
1. 897
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6722106"
/cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231, hTERT-HME1, LNCaP"
/lab_host="EMD10B"
/note="Vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not I; Subtracted with brain, liver, lung, kidney and muscle. Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold. Kristi A. Eglund, James J. Vincent, Robert Strausberg, Bungkok Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins. Manuscript submitted."

ORIGIN

Query Match 30.5%; Score 656; DB 6; Length 897;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 656; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGCTGTACAGGGGCTGCCAGAGCTGAGCCGGGACCGAGGCGGAGACATATGA 60

Db 3 GGGGCTGTACAGGGGCTGCCAGAGCTGAGCCGGGACCGAGGCGGAGACATATGA 62

QY 61 TGAAGCGCTTGGAGTGGAGCGCTGGGGGCTTCTGAGTGGCGCATCTCCCTGCTCT 120

Db 63 TGAAGCGCTTGGAGTGGAGCGCTGGGGGCTTCTGAGTGGCGCATCTCCCTGCTCT 122

QY 121 CTCTCTGTATGACCGGCTGGTGGAGCGATTCGGCACTCGAGCATATTTGGCCAG 180

Db 123 CTCTCTGTATGACCGGCTGGTGGAGCGATTCGGCACTCGAGCATATTTGGCCAG 182

QY 181 TGTGAGAGCTTTCCTGTGGGCTGCGGTRGCCATATGCTCTGTGCCAAGTGTGGCCTGT 240

Db 183 TGTGAGAGCTTTCCTGTGGGCTGCGGTRGCCAATGCTCTGTGCCAAGTGTGGCCTGT 242

QY 241 GACAGCTTACGCGGCTTACCGGAGTTCACCTTCTCAGGCTTGCAGATCTGCGCTACAC 300

Db 243 GACAGCTTACGCGGCTTACCGGAGTTCACCTTCTCAGGCTTGCAGATCTGCGCTACAC 302

QY 301 ACTGAGCTTCTCTTACACCGGAGAGAGAGGAGTGTTCCTGCCAATACGAGGAGACAC 360

Db 303 ACTGAGCTTCTCTTACACCGGAGAGAGAGGAGTGTTCCTGCCAATACGAGGAGACAC 362

QY 361 TGAAGTGTCTACAGTGAAGACAGCTGTATACACAGCTTCTTCCAGGCGCTTAAAGCTGG 420

Db 363 TGAAGTGTCTACAGTGAAGACAGCTGTATACACAGCTTCTTCCAGGCGCTTAAAGCTGG 422

QY 421 AGCTCCCTTCCCTTAAATGACACAGTGGGCTCTGGAAGCACTGAGCTGCCACCTCCACC 480

Db 423 AGCTCCCTTCCCTTAAATGACACAGTGGGCTCTGGAAGCACTGAGCTGCCACCTCCACC 482

QY 481 CGCGCTTGCAGGAGCTCTGCTGTGATGTCTCCGTAAGTGTGTGGTGGTGAAGCCAC 540

Db 483 CGCGCTTGCAGGAGCTCTGCTGTGATGTCTCCGTAAGTGTGTGGTGGTGAAGCCAC 542

QY 541 CGAGCCAGAGGTGTCTTCCGAGCGGCGGAGCATCTGCTGACCTCGCATCTGGATATGTC 600

Db 543 CGAGCCAGAGGTGTCTTCCGAGCGGCGGAGCATCTGCTGACCTCGCATCTGGATATGTC 602

QY 601 CTTCCTGTCTGCCAGGTGGGCCCATCCCTGTTTATGAGCTCATTTGCAGCTCA 656

Db 603 CTTCCTGTCTGCCAGGTGGGCCCATCCCTGTTTATGAGCTCATTTGCAGCTCA 658

RESULT 6
BU689021/c
LOCUS BU689021/c
DEFINITION UI-CP-BCL-ady-f-04-0-UI s1 UI-CP-BCL Homo sapiens cDNA clone
ACCESSION BU689021
VERSION BU689021.1 GI:23546376
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: McCray, PB
McCrack Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.reagen.com) or from Open Biosystems (www.openbiosystems.com).
The following repetitive elements were found in this cDNA sequence: 1-28, >AT-rich#low_complexity
Seq primer: M13 FORWARD
POLYA=yes.
Location/Qualifiers
1. 670

FEATURES
source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-EC1-ady-f-04-0-UI"
/tissue_type="Lung"
/dev_stage="Adult and Fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-EC1"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: Score 1; Site 2: Not 1; UI-CF-EC1 is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AAGTCTTAC.
TAG_ISSUE=Normal Lung Epithelial Cells Tissue nos 369-371 and 380-383
TAG_LIB=UI-CF-EC1
TAG_SEQ=AAGTCTTAC"

ORIGIN

Query Match 29.9%; Score 644; DB 5; Length 670;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1509 GGGGATCCCAACATCAGTCCCGGAGATAGCTGGTCAATGGGCTGATTCATTCGCAAA 1568
Db 661 GGGGATCCCAACATCAGTCCCGGAGATAGCTGGTCAATGGGCTGATTCGCAAA 602

QY 1569 ATCTTCTTCTCTGGGGCTGAGCCGCCCAAAATGCTTAAACCGAGACTTGGAAATCTTA 1628
Db 601 ATCTTCTTCTCTGGGGCTGAGCCGCCCAAAATGCTTAAACCGAGACTTGGAAATCTTA 542

QY 1629 CTCATCCCAATATATATTCCTCAATCTGTATACCAAGTTAGGCTGTGAAGAAAGTAA 1688
Db 541 CTCATCCCAATATATATTCCTCAATCTGTATACCAAGTTAGGCTGTGAAGAAAGTAA 482

QY 1689 GAGGGTGGGGCTTCAGGTCTCAACGGCTTCCCTAACACCCCTCTCTCTGGCCAGGC 1748
Db 481 GAGGGTGGGGCTTCAGGTCTCAACGGCTTCCCTAACACCCCTCTCTCTGGCCAGGC 422

QY 1749 TGGTTCCTCCCACTTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1808
Db 421 TGGTTCCTCCCACTTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 362

QY 1809 CCCAAATTTCCCTCAGTCCCGCACTTCCCTAACCCCGCACTTCCCGCAAGCTCCACA 1868
Db 361 CCCAAATTTCCCTCAGTCCCGCACTTCCCTAACCCCGCACTTCCCGCAAGCTCCACA 302

QY 1869 ACCCTGTTTGAAGCTACCTGAGAGCCAGAACCAAGTCCGCTTCCCAAGCTTTGTC 1928
Db 301 ACCCTGTTTGAAGCTACCTGAGAGCCAGAACCAAGTCCGCTTCCCAAGCTTTGTC 242

QY 1929 CATTTCAGCCCCCAGATATCTGTGTGGGGAAATCTCACACGAAATCTCAGAGAC 1988
Db 241 CATTTCAGCCCCCAGATATCTGTGTGGGGAAATCTCACACGAAATCTCAGAGAC 182

QY 1989 CCCCTGCTGAGCTAAGGAGGCTTATCTCAGAGGGGGGTTTAAAGTCGGTTTGAAT 2048
Db 181 CCCCTGCTGAGCTAAGGAGGCTTATCTCAGAGGGGGGTTTAAAGTCGGTTTGAAT 122

QY 2049 AATGTCGCTTATTTATTTAGGGGGGTAATTTTATATCTGTAAAGTCAATCAGAGT 2108
Db 121 AATGTCGCTTATTTATTTAGGGGGGTAATTTTATATCTGTAAAGTCAATCAGAGT 62

QY 2109 ATATGTTATGTCACAAATTTAAAGGCTTCTATATGTTTA 2152
Db 61 ATATGTTATGTCACAAATTTAAAGGCTTCTATATGTTTA 18

RESULT 7
CB048223
LOCUS
DEFINITION
NISC 5103e11.y1 NCI_CGAP_Px28 Homo sapiens cDNA clone IMAGE:3270644
5', mRNA sequence.
ACCESSION
CB048223
VERSION
CB048223.1 GI:27786510
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
1 (bases 1 to 651)
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
CDNA Library Preparation:
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
info@image.lnl.gov
Plate: LLM8006 row: J column: 21
Seq primer: M13RP1 reverse primer (AB1).
Location/Qualifiers
1..651
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3270644"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI CGAP Px28"
/note="Organ: prostate; Vector: pT73D-Pac (Pharmacia)
with a modified polylinker. Plasmid DNA from the
normalized library NCI_CGAP_Px22 was prepared, and as
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonoids
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and W. Fatima Bonaldi."

FEATURES

source

QY 1462 TCATGCTAGCTTTTCTGTGTGGTGTCTAATATTTGGGTAGGGATCCCAAC 1521
Db 14 TCATGCTAGCTTTTCTGTGTGGTGTCTAATATTTGGGTAGGGATCCCAAC 73

QY 1522 AATCAGGTCCTCGAGATAGCTGATAGGGGTGATTCATTCGCAAAATCTTCTCTCT 1581
Db 74 AATCAGGTCCTCGAGATAGCTGATAGGGGTGATTCATTCGCAAAATCTTCTCTCT 133

QY 1582 GGGGTCGCCCCCAAAATGCTTAAACCGAGACTTGGAAATCTACTCATCCCAATG 1641
Db 134 GGGGTCGCCCCCAAAATGCTTAAACCGAGACTTGGAAATCTACTCATCCCAATG 193

QY 1642 ATATATCCAAATGCTGTACCCCAAGTTAGGGTGTGAAGAAAGTAAAGGCTGGGCTT 1701
Db 194 ATATATCCAAATGCTGTACCCCAAGTTAGGGTGTGAAGAAAGTAAAGGCTGGGCTT 253

ORIGIN

Query Match 29.6%; Score 638; DB 6; Length 651;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 638; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1702	CAGGCTCAAGGGCTTCCCTTAACACACCCCTCTTCTCTTGAGCCAGAGCTGGTTCCCCAC	1761
Db	254	CAGGCTCAAGGGCTTCCCTTAACACACCCCTCTTCTCTTGAGCCAGAGCTGGTTCCCCAC	313
QY	1762	TTGCAGTCCCTCTACTCTCTCTAGAGCTGGGCTGATAGAGCACTGCCAAATTTCC	1821
Db	314	TTGCAGTCCCTCTACTCTCTCTAGAGCTGGGCTGATAGAGCACTGCCAAATTTCC	373
QY	1822	CTACCCCAACTTTTCCCTTACCCCAACTTTTCCCAACAGCTCCACAAACCTGTGTTGGAG	1881
Db	374	CTACCCCAACTTTTCCCTTACCCCAACTTTTCCCAACAGCTCCACAAACCTGTGTTGGAG	433
QY	1882	CTACTGCAGACACAGAAACACAAAGTGCGGTTTTCCCAAGCCTTTGTCCATCTCAGCCCC	1941
Db	434	CTACTGCAGACACAGAAACACAAAGTGCGGTTTTCCCAAGCCTTTGTCCATCTCAGCCCC	493
QY	1942	AGAGTATATCTGTGCTTGGGGATCTCACAGAAACTCAGAGAGCACCCCTGCCTGAGC	2001
Db	494	AGAGTATATCTGTGCTTGGGGATCTCACAGAAACTCAGAGAGCACCCCTGCCTGAGC	553
QY	2002	TAAGGAGGTCCTTATCTCTCAGAGGGGGGTTTAAAGTCCGTTTGCAATAATGCTCTTAT	2061
Db	554	TAAGGAGGTCCTTATCTCTCAGAGGGGGGTTTAAAGTCCGTTTGCAATAATGCTCTTAT	613
QY	2062	TTATTATCGGGGATATATTTTATATCTGTAAGTAGC	2099
Db	614	TTATTATCGGGGATATATTTTATATCTGTAAGTAGC	651

[illegible]

```

FEATURES
Source
Location/Qualifiers
1. 916
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6205362"
/sex="male"
/tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
/clone_1ib="Lupski_sciatic nerve"
/note="Vector: pCMV-SPORT2 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TTCAGCCACGCTCCG-3' and
5'-GACTGATGTTCTAAGTCGAGCGCCGCCCT(15)-3'. Size selected >

```

ORIGIN

1 kb for average insert length 1.87 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."

Query Match	28.7%	Score 617;	DB 5;	Length 916;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 617; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1101	TAGCCTCTGAGTGAACAACCTGAGGAAGAGGTTTTTGGAGCTGAATTAATCAAGCA	1160
Db	1	TAGCCTCTGAGTGAACAACCTGAGGAAGAGGTTTTTGGAGCTGAATTAATCAAGTCA	60
QY	1161	CTGAGTTTCCATCTCTAAGCCCTTAACTGACGCTTGGTTAATGTAGCTTTCGATG	1220
Db	61	CTGAGTTTCCATCTCTAAGCCCTTAACTGACGCTTGGTTAATGTAGCTTTCGATG	120
QY	1221	GGAGTTTCTAGAGTAAGAACACTCCTGCATGGGATTTGAACATAGAAGTATTTGGAG	1280
Db	121	GGAGTTTCTAGAGTAAGAACACTCCTGCATGGGATTTGAACATAGAAGTATTTGGAG	180
QY	1281	GGAAGAGTCTCTGAGGGGCAACACAGAAGAACAGGTCCCTCAGCCCAAGCACTGTCTT	1340
Db	181	GGAAGAGTCTCTGAGGGGCAACACAGAAGAACAGGTCCCTCAGCCCAAGCACTGTCTT	240
QY	1341	TTTGTGATCATACCCCTCTTACCTTTTATCAGGATGTGGCTGTGTCTTCTGTG	1400
Db	241	TTTGTGATCATACCCCTCTTACCTTTTATCAGGATGTGGCTGTGTCTTCTGTG	300
QY	1401	CCATCAAGAGACACAGGCAATTAAATATTAACTTAATTAAACAAAGTAGAAGGA	1460
Db	301	CCATCAAGAGACACAGGCAATTAAATATTAACTTAATTAAACAAAGTAGAAGGA	360
QY	1461	ATCATTTGCTAGCTTTTCTGTGTGTGTCTAAATTTTGGGTAGGATGCCCAA	1520
Db	361	ATCATTTGCTAGCTTTTCTGTGTGTGTCTAAATTTTGGGTAGGATGCCCAA	420
QY	1521	CAATCAGGTCCCTGAGATAGCTGTCTAATGGGCTGATCATGTGCCAATCTTTCTCC	1580
Db	421	CAATCAGGTCCCTGAGATAGCTGTCTAATGGGCTGATCATGTGCCAATCTTTCTCC	480
QY	1581	TGGGGTCTGGCCCCCAAAATGCTTAACCCAGACCTTGGAAATTTCACTCATCCCAAT	1640
Db	481	TGGGGTCTGGCCCCCAAAATGCTTAACCCAGACCTTGGAAATTTCACTCATCCCAAT	540
QY	1641	GATTAATTCCAAATGCTGTTAACCCAAAGTTAAGGTTGAAGAAAGTTAAGAGGTTGGGCT	1700
Db	541	GATTAATTCCAAATGCTGTTAACCCAAAGTTAAGGTTGAAGAAAGTTAAGAGGTTGGGCT	600
QY	1701	TCAGGTCTCAACGGCTT 1717	
Db	601	TCAGGTCTCAACGGCTT 617	

RESULT 9	
B0950805	
LOCUS	B0950805 959 bp mRNA linear EST 21-AUG-2002
DEFINITION	AGENCOURT_8842232 lupski_sciatic_nerve Homo sapiens cDNA clone
ACCESSION	IMAGE:6204253 5', mRNA sequence.
VERSION	B0950805
KEYWORDS	B0950805.1 GI:2236283
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 959) NIH-MGC http://mgc.ncl.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D.
TITLE	
AUTHORS	
JOURNAL	
COMMENT	

Db 301 TCCCTTCCCTATGACACAGTGGTCTGAGAGCAATGGCTCTCCACCTCCACCCG 360
Qy 484 GCTTCGCGGGGCTCTGCTGTGAGTCTCCGTAAGTGTGTGTGAGCCGCA 543
Db 361 GCTTCGCGGGGCTCTGCTGTGAGTCTCCGTAAGTGTGTGTGAGCCGCA 420
Qy 544 GGGCAGGGGTGTTCCGGGCGGGGCACTGCTGACCTCGCATCTGATATGTCCTT 603
Db 421 GGGCAGGGGTGTTCCGGGCGGGGCACTGCTGACCTCGCATCTGATATGTCCTT 480
Qy 604 CTTGCTGCTCCAGTGGCCCATCTGTTTATGAGCTCCATTTGCTCAGCTCAGCCAGTC 663
Db 481 CTTGCTGCTCCAGTGGCCCATCTGTTTATGAGCTCCATTTGCTCAGCTCAGCCAGTC 540
Qy 664 T 664
Db 541 T 541

RESULT 11
LOCUS CN373214 581 bp mRNA linear EST 16-MAY-2004
DEFINITION 1700532189001 GRN ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN373214
VERSION CN373214.1 GI:47373148
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 581)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebrowski, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 581 Std Error: 0.00.
Location/Qualifiers
1..581
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, cell lines H1, H7, and
H9"
/clone_11b="GRN ES"
/note="oligo dt primed, full-length enriched cDNA library
from undifferentiated hES cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"

ORIGIN
Query Match 24.5%; Score 528; DB 7; Length 581;
Best Local Similarity 100.0%; Pred. No. 3,6e-272; Indels 0; Gaps 0;
Matches 528; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1161 CTTGTTCCCTCTTAAGCCCTTAACCTGACGCTGTTATGATGCTCTTGACATG 1220
Db 39 CTTGTTCCCTCTTAAGCCCTTAACCTGACGCTGTTATGATGCTCTTGACATG 98
Qy 1221 GGAAGTTTCTAGATGAACAATCTCTCAAGGATTTGAACATATGAAGTATTTTAGG 1280
Db 99 GGAAGTTTCTAGATGAACAATCTCTCAAGGATTTGAACATATGAAGTATTTTAGG 158
Qy 1281 GGAAGTCTCTAGAGGGGCAACACAGAAGACAGTCCCTCAGCCACAGCACTGCTT 1340

Db 159 GGAAGTCTCTAGAGGGGCAACACAGAAGACAGTCCCTCAGCCACAGCACTGCTT 218
Qy 1341 TTTGCTGATCCACCCCTCTTAACCTTTATCAAGATGTGGCTGTGCTCTGTG 1400
Db 219 TTTGCTGATCCACCCCTCTTAACCTTTATCAAGATGTGGCTGTGCTCTGTG 278
Qy 1401 CCATCAGAGACACAGGCACTTAAATATTAACTTATTTTAAACAAGTAGAAGGA 1460
Db 279 CCATCAGAGACACAGGCACTTAAATATTAACTTATTTTAAACAAGTAGAAGGA 338
Qy 1461 ATCCATTTGCTAGCTTTTCTGTGTGCTATTAATTTTGGTAGGGATGCCCA 1520
Db 339 ATCCATTTGCTAGCTTTTCTGTGTGCTATTAATTTTGGTAGGGATGCCCA 398
Qy 1521 CAATCAGTCCCTGAGATAGCTGTGATTTGAGGCTGATCATTCAGAAATCTTCTCC 1580
Db 399 CAATCAGTCCCTGAGATAGCTGTGATTTGAGGCTGATCATTCAGAAATCTTCTCC 458
Qy 1581 TGGGGTCTGGCCCCCAAAATGCTTAACCCAGAGACCTTGGAAATCTCATCCCAAT 1640
Db 459 TGGGGTCTGGCCCCCAAAATGCTTAACCCAGAGACCTTGGAAATCTCATCCCAAT 518
Qy 1641 GATTAATCCAAATGCTTTACCCCAAGTTAGGATTTGAAGGAGTA 1688
Db 519 GATTAATCCAAATGCTTTACCCCAAGTTAGGATTTGAAGGAGTA 566

RESULT 12
LOCUS BG469586 589 bp mRNA linear EST 21-MAR-2001
DEFINITION 602533622F1 NIH_MGC_15 Homo sapiens cDNA IMAGE:4661500 5',
mRNA sequence.
ACCESSION BG469586
VERSION BG469586.1 GI:13401861
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 589)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
DNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LNCM1460 row: K column: 05
High quality sequence stop: 587.
Location/Qualifiers
1..589
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_11b="IMAGE:4661500"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_11b="NIH_MGC_15"
/note="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCAGCAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN

Query Match 22.8%; Score 491; DB 4; Length 589;
Best Local Similarity 100.0%; Pred. No. 3.1e-252; Indels 0; Gaps 0;
Matches 491; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1190 CTGACGCTCTGTTTAATGTAAGTCTTGGATGGAGTTTCAAGATGAACAACCTCCAT 1249
Db 2 CTGACGCTCTGTTTAATGTAAGTCTTGGATGGAGTTTCAAGATGAACAACCTCCAT 61

QY 1250 GGGATTTGAACATGTAAGTCTTGGATGGAGTTTCAAGATGAACAACCTCCAT 1309
Db 62 GGGATTTGAACATGTAAGTCTTGGATGGAGTTTCAAGATGAACAACCTCCAT 121

QY 1310 ACCAGTCCCTCCAGCCACAGACTGCTTTTGTGATCAACCCCTCTTACCTTT 1369
Db 122 ACCAGTCCCTCCAGCCACAGACTGCTTTTGTGATCAACCCCTCTTACCTTT 181

QY 1370 ATCAGATGTCGCTGTTGCTTCTTGTGATCAACAGACACAGGATTTAAAT 1429
Db 182 ATCAGATGTCGCTGTTGCTTCTTGTGATCAACAGACACAGGATTTAAAT 241

QY 1430 TTAATTTATTTATTAACAAGTGAAGGATTCATGCTTCTTCTTCTTCTTCTT 1489
Db 242 TTAATTTATTTATTAACAAGTGAAGGATTCATGCTTCTTCTTCTTCTTCTT 301

QY 1490 CTAAATTTGGGATGGGATGGGATGCCCAACATCAGTCCCTGAGATGCTGAT 1549
Db 302 CTAAATTTGGGATGGGATGGGATGCCCAACATCAGTCCCTGAGATGCTGAT 361

QY 1550 TGGGCTGATGATGCGCAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1609
Db 362 TGGGCTGATGATGCGCAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 421

QY 1610 CAGACCTTGAATTTCTACTCAATCCCAATGATTAATCCAAATGCTTTAACCAGTT 1669
Db 422 CAGACCTTGAATTTCTACTCAATCCCAATGATTAATCCAAATGCTTTAACCAGTT 481

QY 1670 AGGCTGTGA 1680
Db 482 AGGCTGTGA 492

RESULT 13
B0942028 875 bp mRNA linear EST 21-AUG-2002
LOCUS AGENCOURT_8817111 lupski_sciatic nerve Homo sapiens cDNA clone
DEFINITION IMAGE:6202754 5', mRNA sequence.
ACCESSION B0942028
VERSION B0942028.1 GI:22357506
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 875)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: L1M13621 row: f column: 03
High quality sequence stop: 417.
location/Qualifiers
1. 875
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

FEATURES
source

/clone="IMAGE:6202754"
/sex="male"
/tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="PH10B"
/clone_lib="lupski_sciatic nerve"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site 1:
NotI; Site 2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCAAGGCTCG-3' and
5'-GACTGTTCTTAATGCGACGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

Query Match 22.1%; Score 475; DB 5; Length 875;
Best Local Similarity 100.0%; Pred. No. 1.4e-243; Indels 0; Gaps 0;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

QY 1285 GAGTCTGAGGGGCAACACAAAGACAGGCTCCAGCCACAGACGTCCTTTT 1344
Db 1 GAGTCTGAGGGGCAACACAAAGACAGGCTCCAGCCACAGACGTCCTTTT 60

QY 1345 CTGATCAACCCCTCTTACCTTTATCAGATGAGGCTGTCCTTCTGTTGCCAT 1404
Db 61 CTGATCAACCCCTCTTACCTTTATCAGATGAGGCTGTCCTTCTGTTGCCAT 120

QY 1405 CACAGAGACAGGATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1464
Db 121 CACAGAGACAGGATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 180

QY 1465 ATTGCTACCTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1524
Db 181 ATTGCTACCTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 240

QY 1525 CAGTCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1584
Db 241 CAGTCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300

QY 1585 GTCTGCCCCCAAAATGCTTAACCCAGACCTTGAATTTCTATCTATCCAAATGATA 1644
Db 301 GTCTGCCCCCAAAATGCTTAACCCAGACCTTGAATTTCTATCTATCCAAATGATA 360

QY 1645 ATTCCAATGCTTTTACCAAGTTAGGTTGTAAGAAAGTGAAGGTTGAG 1704
Db 361 ATTCCAATGCTTTTACCAAGTTAGGTTGTAAGAAAGTGAAGGTTGAG 420

QY 1705 GTCTCAAGGCTTCCCTTAACCAACCCCTCTTCTTGGCCCAAGCTTGGCTTCC 1759
Db 421 GTCTCAAGGCTTCCCTTAACCAACCCCTCTTCTTGGCCCAAGCTTGGCTTCC 475

RESULT 14
BM914562 1060 bp mRNA linear EST 12-MAR-2002
LOCUS BM914562
DEFINITION AGENCOURT_6615475 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5480245
ACCESSION BM914562
VERSION BM914562.1 GI:19364941
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1060)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Mark Watson
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.jnl.gov>
 Plate: LNCM2002 row: m column: 14
 High quality sequence stop: 485.

FEATURES

source

1..1060
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5480245"
 /lab_host="PH10B (phage-resistant)"
 /clone_1ib="NIH_MGC_113"
 /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCAAGAG(G). Library constructed by Ling Hong in the
 Laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN

Query Match 22.0%; Score 474; DB 5; Length 1060;
 Best Local Similarity 100.0%; Pred. No. 4,7e-243;

Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 360 CTGGAGGCTCTGACAGTGAAGACAGCTTATGACACGCTTCTGCGACGGCCCTTAAGCTTG 419
   |||||
DB 1 CTGGAGGCTCTGACAGTGAAGACAGCTTATGACACGCTTCTGCGACGGCCCTTAAGCTTG 60
QY 420 GAGCTCCCTTCCCTAATGACACAGTGGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 479
   |||||
DB 61 GAGCTCCCTTCCCTAATGACACAGTGGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
QY 480 CCGCGCTCTGCGGGGCTCTGCTGTGATGTCTCCGTACGTGTGTGTGTGTGTGTGTGTGTGT 539
   |||||
DB 121 CCGCGCTCTGCGGGGCTCTGCTGTGATGTCTCCGTACGTGTGTGTGTGTGTGTGTGTGTGT 180
QY 540 CCGAGGCGGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 599
   |||||
DB 181 CCGAGGCGGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
QY 600 CCTTCCTGCTGCCAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 659
   |||||
DB 241 CCTTCCTGCTGCCAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
QY 660 AGCTGTGTCTGCTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 719
   |||||
DB 301 AGCTGTGTCTGCTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
QY 720 CTACACAGGTAGTATTTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 779
   |||||
DB 361 CTACACAGGTAGTATTTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
QY 780 GCACATTTGGGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 833
   |||||
DB 421 GCACATTTGGGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 474

```

RESULT 15

BX098291

LOCUS

DERIVATION

ACCESSION

VERSION

KEYWORDS

SOURCE

BX098291 515 bp mRNA 1linear EST 04-FEB-2003
 IMAGP988P04693; IMAGE:308595, mRNA sequence.
 BX098291.1 GI:27843586
 Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE

1 (bases 1 to 515)

AUTHORS

Ebert, L., Hell, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
 Radloff, U., Schneider, D. and Korn, B.

TITLE

Human unigeneset - RZPD

JOURNAL

Unpublished (2003)

COMMENT

Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
 RZPD: IMAGP988P04693.
 RZPDLIB: I.M.A.G.E. cDNA Clone Collection;
<http://www.rzpd.de/ClonesCards/cgi-bin/showLib.pl.cgi?response?libNo=972> Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Heubnerweg 6, D-14059 Berlin, Germany
 Tel: +49 30 32639 101
 Fax: +49 30 32639 111
 www.rzpd.de
 This clone is available royalty-free from RZPD;
 contact RZPD (clone@rzpd.de) for further information. Seq primer:
 M13r, Primer sequence: TTTCCACAGGAAACAGCTATGAC.

FEATURES

source

1..515
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGP988P04693; IMAGE:308595"
 /dev_stage="19 weeks"
 /lab_host="PH10B (ampicillin resistant)"
 /clone_1ib="Soares_fetal_lung_NbHL19W"
 /note="Organ: lung; Vector: pTZ19 (Pharmacia) with a
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer
 (5'-TGTTACCACTGAAAGTGGAGGCGGCGGCAATTTTCTTTT-3'),
 double-stranded cDNA was size selected, ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pTZ19 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M. Fatima Bonaldo. This library was constructed
 from the same fetus as the fetal heart library, Soares
 fetal heart NbHL19W."

ORIGIN

Query Match 21.8%; Score 470; DB 5; Length 515;
 Best Local Similarity 100.0%; Pred. No. 6.4e-241;

Matches 470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1605 TAACCCAGGACCTTGAAATTTCTACTCATCCCAATGATATTCAAATGCTGTACCA 1664
   |||||
DB 34 TAACCCAGGACCTTGAAATTTCTACTCATCCCAATGATATTCAAATGCTGTACCA 93
QY 1665 AGTTAGGGTGTGGAAGAGTGAAGGGTGGGGCTTCAGGTCCTCAAGGCTTCCCTAAC 1724
   |||||
DB 94 AGTTAGGGTGTGGAAGAGTGAAGGGTGGGGCTTCAGGTCCTCAAGGCTTCCCTAAC 153
QY 1725 CACCCCTCTCTCTTGGGCCAGGCTGGTCCGCCCACTTCCCACTCCCTCTACTCTCTCT 1784
   |||||
DB 154 CACCCCTCTCTCTTGGGCCAGGCTGGTCCGCCCACTTCCCACTCCCTCTACTCTCTCT 213
QY 1785 AGGACTGGGCTGATGAAGGCACTGCCCCAATTTCCCTTACCCCACTTCCCTTACCC 1844
   |||||
DB 214 AGGACTGGGCTGATGAAGGCACTGCCCCAATTTCCCTTACCCCACTTCCCTTACCC 273
QY 1845 CCACTTTTCCCAAGGCTCCCAACCCCTGTTTGAAGTACTGCAAGACCAAGACCA 1904
   |||||
DB 274 CCACTTTTCCCAAGGCTCCCAACCCCTGTTTGAAGTACTGCAAGACCAAGACCA 333
QY 1905 AGTGGGTTTCCCAAGGCTTGTTCATCTCAGCCCAAGAGATATCTGTGCTGGGGA 1964
   |||||

```

Db	334	AGTGGGTTTCCCAAGCCTTTGTCCATCTCAGCCCCCAGAGTATATCTGTGCTTGAGAA	393
QY	1365	TCTCACAAGAACTCAGAGACACCCCTGCTGAGCTAAGGAGGTCTTATCTTCAGG	2024
Db	394	TCTCACAAGAACTCAGAGACACCCCTGCTGAGCTAAGGAGGTCTTATCTTCAGG	453
QY	2025	GGGGGTTTAAAGTCCGTTTGCAATATATGTGCTTATTATTATTAGCGGGG	2074
Db	454	GGGGGTTTAAAGTCCGTTTGCAATATATGTGCTTATTATTATTAGCGGGG	503

Search completed: February 8, 2005, 21:26:58
Job time : 7013.66 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 8, 2005, 09:49:12 ; Search time 9229.62 Seconds
(without alignment(s))
11250.684 Million cell updates/sec

Title: US-09-841-894A-15

Perfect score: 2143
Sequence: 1 ACCAGGGCGCTGCCAGAGCT.....AAGCTTCTTATATGTTTA 2143

Scoring table: ~~OLIGO~~WUC*
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:.*
2: gb_hlg:.*
3: gb_in:.*
4: gb_om:.*
5: gb_ov:.*
6: gb_pat:.*
7: gb_ph:.*
8: gb_pl:.*
9: gb_pr:.*
10: gb_ro:.*
11: gb_scs:.*
12: gb_sy:.*
13: gb_un:.*
14: gb_vl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2143	100.0	2143	6 AR112294	AR112294 Sequence
2	1972	92.0	2152	6 AR112295	AR112295 Sequence
3	1970	91.9	3306	9 BC050416	BC050416 Homo Sapi
4	1916	89.4	2904	6 AR278710	AR278710 Sequence
5	1916	89.4	2904	6 AR400442	AR400442 Sequence
6	1916	89.4	2904	6 AR405709	AR405709 Sequence
7	1916	89.4	2904	6 AR564089	AR564089 Sequence
8	1916	89.4	2904	6 AX200994	AX200994 Sequence
9	1916	89.4	2904	6 AX267729	AX267729 Sequence
10	1900	88.7	3320	6 AX327336	AX327336 Sequence
11	1796	83.8	4034	6 AR278711	AR278711 Sequence
12	1796	83.8	4034	6 AR400443	AR400443 Sequence
13	1796	83.8	4034	6 AR405710	AR405710 Sequence
14	1796	83.8	4034	6 AR564090	AR564090 Sequence
15	1796	83.8	4034	6 AR564095	AR564095 Sequence
16	1796	83.8	4034	6 AX267730	AX267730 Sequence
17	1764	82.3	4894	6 AR278709	AR278709 Sequence
18	1764	82.3	4894	6 AR400441	AR400441 Sequence
19	1764	82.3	4894	6 AR405708	AR405708 Sequence

20	1764	82.3	4894	6 AR564088	AR564088 Sequence
21	1764	82.3	4894	6 AX200993	AX200993 Sequence
22	1764	82.3	4894	6 AX267728	AX267728 Sequence
23	1739	81.1	3410	6 BD242022	BD242022 Compounds
24	1739	81.1	3410	6 AR237205	AR237205 Sequence
25	1739	81.1	3410	6 AR278229	AR278229 Sequence
26	1739	81.1	3410	6 AR366925	AR366925 Sequence
27	1739	81.1	3410	6 AR370821	AR370821 Sequence
28	1739	81.1	3410	6 AR392326	AR392326 Sequence
29	1739	81.1	3410	6 AR399961	AR399961 Sequence
30	1739	81.1	3410	6 AR405228	AR405228 Sequence
31	1739	81.1	3410	6 AR439432	AR439432 Sequence
32	1739	81.1	3410	6 AR563608	AR563608 Sequence
33	1739	81.1	3410	6 AX106329	AX106329 Sequence
34	1739	81.1	3410	6 AX140620	AX140620 Sequence
35	1739	81.1	3410	6 AX200480	AX200480 Sequence
36	1739	81.1	3410	6 AX267136	AX267136 Sequence
37	1739	81.1	3410	6 AX429961	AX429961 Sequence
38	1739	81.1	3410	6 BD070258	BD070258 Compounds
39	1739	81.1	3410	9 AY033593	AY033593 Homo Sapi
40	1651	77.0	6976	6 AR278712	AR278712 Sequence
41	1651	77.0	6976	6 AR400444	AR400444 Sequence
42	1651	77.0	6976	6 AR405711	AR405711 Sequence
43	1651	77.0	6976	6 AR564091	AR564091 Sequence
44	1651	77.0	6976	6 AX200996	AX200996 Sequence
45	1651	77.0	6976	6 AX267731	AX267731 Sequence

ALIGNMENTS

RESULT 1
AR112294
LOCUS AR112294 Sequence 15 from patent US 6130043.
DEFINITION AR112294
ACCESSION AR112294
VERSION AR112294.1 GI:14092194
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2143)
AUTHORS Billing-Medel,P.A., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D., Roberts-Rapp,L., Russell,J.C., Stroupe,S.D. and Yu,H.
TITLE Regents and methods useful for detecting diseases of the prostate
JOURNAL Patent: US 6130043-A 15 10-OCT-2000;
FEATURES
source
1..2143
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 2143; DB 6; Length 2143;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 2143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCAGGGCGCTGCCAGAGCTGAGCCGGGACCGAGGCCGAGACCTATGATGAAGCG 60
1 ACCAGGGCGCTGCCAGAGCTGAGCCGGGACCGAGGCCGAGACCTATGATGAAGCG 60
DB 1 ACCAGGGCGCTGCCAGAGCTGAGCCGGGACCGAGGCCGAGACCTATGATGAAGCG 60
1 ACCAGGGCGCTGCCAGAGCTGAGCCGGGACCGAGGCCGAGACCTATGATGAAGCG 60
QY 61 TTCGATGGGCGAGCTGGGGCTGTTCTGCACTGCGCCATCTCCCTGCTCTCTG 120
61 TTCGATGGGCGAGCTGGGGCTGTTCTGCACTGCGCCATCTCCCTGCTCTCTG 120
DB 61 TTCGATGGGCGAGCTGGGGCTGTTCTGCACTGCGCCATCTCCCTGCTCTCTG 120
61 TTCGATGGGCGAGCTGGGGCTGTTCTGCACTGCGCCATCTCCCTGCTCTCTG 120
QY 121 TCATGGACCGGCTGGTGCAGCGATTGGCACTCGAGCAGTCTATTGGCAGTGGCAG 180
121 TCATGGACCGGCTGGTGCAGCGATTGGCACTCGAGCAGTCTATTGGCAGTGGCAG 180
DB 121 TCATGGACCGGCTGGTGCAGCGATTGGCACTCGAGCAGTCTATTGGCAGTGGCAG 180
121 TCATGGACCGGCTGGTGCAGCGATTGGCACTCGAGCAGTCTATTGGCAGTGGCAG 180
QY 181 CTTTCCCTGTGCTGCGGCTGCGGTCGCACATGCTGTCCACAGTGTGCGGTCGACGCTT 240
181 CTTTCCCTGTGCTGCGGCTGCGGTCGCACATGCTGTCCACAGTGTGCGGTCGACGCTT 240
DB 181 CTTTCCCTGTGCTGCGGCTGCGGTCGCACATGCTGTCCACAGTGTGCGGTCGACGCTT 240
181 CTTTCCCTGTGCTGCGGCTGCGGTCGCACATGCTGTCCACAGTGTGCGGTCGACGCTT 240

QY 241 CAGCCGCCCTCAGCGGGTTACCTTCTGAGCCCTGAGATCTTGCCTTACACACTGACCT 300
DB 241 CAGCCGCCCTCAGCGGGTTACCTTCTGAGCCCTGAGATCTTGCCTTACACACTGACCT 300
QY 301 CCTTTCACCAACCGGAG 360
DB 301 CCTTTCACCAACCGGAG 360
QY 361 CTAG 420
DB 361 CTAG 420
QY 421 TCCCTAATGACACAGTGGGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 421 TCCCTAATGACACAGTGGGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 481 GCGGGGCTCTGCGTGTATGTCTCCGTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
DB 481 GCGGGGCTCTGCGTGTATGTCTCCGTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
QY 541 GGGTGTCTCCGGGCGGGGCGATCTGCTGAGACCTGCGCATCTCGGATGATGATGATGATG 600
DB 541 GGGTGTCTCCGGGCGGGGCGATCTGCTGAGACCTGCGCATCTCGGATGATGATGATGATG 600
QY 601 TGTCTCCAGAGTGGCCCATCTCTGTTTATGAGGCTCCATTTGATGAGAGAGAGAGAGAG 660
DB 601 TGTCTCCAGAGTGGCCCATCTCTGTTTATGAGGCTCCATTTGATGAGAGAGAGAGAGAG 660
QY 661 CTGCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
DB 661 CTGCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
QY 721 TAGATTTTGAACAAG 780
DB 721 TAGATTTTGAACAAG 780
QY 781 GGTGAG 840
DB 781 GGTGAG 840
QY 841 CCGGCTGGCCGCGCATGTTCTGTTGCTGCGCAAGATGATGATGATGATGATGATGATGATG 900
DB 841 CCGGCTGGCCGCGCATGTTCTGTTGCTGCGCAAGATGATGATGATGATGATGATGATGATG 900
QY 901 GCTGCTGAGAGTGTGTGAGCTGACAGCTGAGGAGGCTGAGGAGGCTGCTCTCTCTCCGAG 960
DB 901 GCTGCTGAGAGTGTGTGAGCTGACAGCTGAGGAGGCTGAGGAGGCTGCTCTCTCTCCGAG 960
QY 961 TCTCTAGAGGCTGCTGAGCTGAGAGGCTTCCAGAGAGAGGCTTCAAGTCTGAGCTTATACAGG 1020
DB 961 TCTCTAGAGGCTGCTGAGCTGAGAGGCTTCCAGAGAGAGGCTTCAAGTCTGAGCTTATACAGG 1020
QY 1021 AGGCGCAAGAGAGGCTTCCATGACCTGAGATGCGGAGCTCTGAGTGTGATTAACCAAGCTCA 1080
DB 1021 AGGCGCAAGAGAGGCTTCCATGACCTGAGATGCGGAGCTCTGAGTGTGATTAACCAAGCTCA 1080
QY 1081 GGGTTTAAAG 1140
DB 1081 GGGTTTAAAG 1140
QY 1141 AAAGCTAGTCACTGTGTTTCCATCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
DB 1141 AAAGCTAGTCACTGTGTTTCCATCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
QY 1201 GCTCTTGAAG 1260
DB 1201 GCTCTTGAAG 1260
QY 1261 TTATTTTGAAG 1320
DB 1261 TTATTTTGAAG 1320
QY 1321 AGCACTGTCTTTTGTCTGATCAACCCCTCTTAACTTTTATCAGAGATGAGCTGTGTGG 1380

DB 1321 AGCACTGTCTTTTGTCTGATCAACCCCTCTTAACTTTTATCAGAGATGAGCTGTGTGG 1380
QY 1381 TCTTTCTGTTTCCATCAACAGAGACAGGCAATTTAAATTTTAACTTATTTTAAACA 1440
DB 1381 TCTTTCTGTTTCCATCAACAGAGACAGGCAATTTAAATTTTAACTTATTTTAAACA 1440
QY 1441 AGTAAAG 1500
DB 1441 AGTAAAG 1500
QY 1501 GGGATCCCAACAAATAGAGTCCCTGAGATGAGTGTGATGAGTGTGATGATGATGATGATG 1560
DB 1501 GGGATCCCAACAAATAGAGTCCCTGAGATGAGTGTGATGAGTGTGATGATGATGATGATG 1560
QY 1561 TCTTCTTCTCCGAGAGTCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1620
DB 1561 TCTTCTTCTCCGAGAGTCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1620
QY 1621 TCATCCCAAT 1680
DB 1621 TCATCCCAAT 1680
QY 1681 AGGGTGGGCTTCCAGAGTCTCAACAGGCTTCCCTAACCAACCTCTTCTTCTGAGGCGGCT 1740
DB 1681 AGGGTGGGCTTCCAGAGTCTCAACAGGCTTCCCTAACCAACCTCTTCTTCTGAGGCGGCT 1740
QY 1741 GGTTCGCCCACTTCACTCCCTCTACTCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
DB 1741 GGTTCGCCCACTTCACTCCCTCTACTCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
QY 1801 CCAAAATTTTCCCTTACCCCACTTTCCTTCCCACTTTCCTTCCCACTTTCCTTCCCACTTTC 1860
DB 1801 CCAAAATTTTCCCTTACCCCACTTTCCTTCCCACTTTCCTTCCCACTTTCCTTCCCACTTTC 1860
QY 1861 CCTGTTTGAAGTCTGAG 1920
DB 1861 CCTGTTTGAAGTCTGAG 1920
QY 1921 ATCTCAGCCGCCAGAGATATCTGTGCTTGGGAGATCTCAACAGAAATCTCAGAGAGAGAGAG 1980
DB 1921 ATCTCAGCCGCCAGAGATATCTGTGCTTGGGAGATCTCAACAGAAATCTCAGAGAGAGAGAG 1980
QY 1981 CCTGCGTGAAGTCTGAG 2040
DB 1981 CCTGCGTGAAGTCTGAG 2040
QY 2041 ATGTGCTTATTTTATTTTATGAG 2100
DB 2041 ATGTGCTTATTTTATTTTATGAG 2100
QY 2101 TTAATGTTATGAG 2160
DB 2101 TTAATGTTATGAG 2160
RESULT 2
AR112295 2152 bp DNA linear PAT 16-MAY-2001
LOCUS AR112295
DEFINITION Sequence 16 from patent US 6130043.
ACCESSION AR112295
VERSION AR112295.1 GI:14092195
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2152)
AUTHORS Billing-Medel, P.A., Cohen, M., Colpites, T.L., Friedman, P.N.,
Gordon, J., Granados, E.N., Hodges, S.C., Klaes, M.R., Kirschchall, J.D.,
Roberts-Rapp, L., Russell, J.C., Stroupe, S.D., and Yu, H.
TITLE Reagents and methods useful for detecting diseases of the prostate
JOURNAL Patent: US 6130043-A 16 10-OCT-2000;
FEATURES Location/Qualifiers

source 1..2152
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 92.0%; Score 1972; DB 6; Length 2152;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2142; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

ORIGIN

1 ACCAGGGGCTGCCAGAGCTGAGCCGGGACCGAGGCCCGAGACACTATGATGAAGCG 60
9 ACCAGGGGCTGCCAGAGCTGAGCCGGGACCGAGGCCCGAGACACTATGATGAAGCG 68
61 TTCGATGGGCAAGCCGCGGCTGTTCCCTGACAGGCGCATCTCCCGGCTCTCTCTCG 120
69 TTCGATGGGCAAGCCGCGGCTGTTCCCTGACAGGCGCATCTCCCGGCTCTCTCTCG 128
121 TCATGAGACCGGCTGGTGCAGCGATTCGACACTGAGCAGTCTATTTGGCCAGTGGCAG 180
129 TCATGAGACCGGCTGGTGCAGCGATTCGACACTGAGCAGTCTATTTGGCCAGTGGCAG 188
181 CTTTCCCTGTGGCTGCCGCTGCAATGCTCTGCCAGTGTGCGGTGGTGAAGCTT 240
189 CTTTCCCTGTGGCTGCCGCTGCAATGCTCTGCCAGTGTGCGGTGGTGAAGCTT 248
241 CAGCGGCGCTCAACCGGCTTCACTTCTGAGCCCTGAGATCCGCTTACAGCTGGCCT 300
249 CAGCGGCGCTCAACCGGCTTCACTTCTGAGCCCTGAGATCCGCTTACAGCTGGCCT 308
301 CCCTTACCAACCGGAGAGAGAGAGTCTCTGCCCAATACGAGGGGACACTGAGAGTG 360
309 CCCTTACCAACCGGAGAGAGAGAGTCTCTGCCCAATACGAGGGGACACTGAGAGTG 368
361 CTAGAGTGAAGACAGCTGATGACAGCTTCTGTCAGAGCCCTTAAAGCTGAGCTCCT 420
369 CTAGAGTGAAGACAGCTGATGACAGCTTCTGTCAGAGCCCTTAAAGCTGAGCTCCT 428
421 TCCCTAATGAGACAGTGGGTGCTGAGAGAGTGGCCTGCTCCACCTCCACCGGCTCT 480
429 TCCCTAATGAGACAGTGGGTGCTGAGAGAGTGGCCTGCTCCACCTCCACCGGCTCT 488
481 GCGGGGCGCTCTGCTGTGATGTCCTCGTACGTGTGGTGGTGAAGCCACCGAGGCA 540
489 GCGGGGCGCTCTGCTGTGATGTCCTCGTACGTGTGGTGGTGAAGCCACCGAGGCA 548
541 GGGTGGTTCGAGGCGGGGCACTGCTGAGACCTGCGCATCTGATAGTGCCTTCTGTC 600
549 GGGTGGTTCGAGGCGGGGCACTGCTGAGACCTGCGCATCTGATAGTGCCTTCTGTC 608
601 TGTCCAGGTGGCCCATGCTGTTTATGAGGCTCCATTTGCCAGCTCAAGCCAGTCTGTA 660
609 TGTCCAGGTGGCCCATGCTGTTTATGAGGCTCCATTTGCCAGCTCAAGCCAGTCTGTA 668
661 CTGCTAATATGATGTCGCGCAGGCTGGTCTGGTCCCATTTACTTTGCTACACAG 720
669 CTGCTAATATGATGTCGCGCAGGCTGGTCTGGTCCCATTTACTTTGCTACACAG 728
721 TAGATATTGACAAGAGCGACTTGGCCAAATACAGCGTGAAGAACTTCCAGACACTTGG 780
729 TAGATATTGACAAGAGCGACTTGGCCAAATACAGCGTGAAGAACTTCCAGACACTTGG 788
781 GGTGAGAGGCGCTGCTCACTGAGGCTCCCACTCCCGCTCTGTAGAGCCCATAGGGCTGC 840
789 GGTGAGAGGCGCTGCTCACTGAGGCTCCCACTCCCGCTCTGTAGAGCCCATAGGGCTGC 848
841 CCGGCTGGGCGCGCAGTTTCTGTGCTGCGCAAGTAAATGAGCTCTGTGCGCACCTGT 900
849 CCGGCTGGGCGCGCAGTTTCTGTGCTGCGCAAGTAAATGAGCTCTGTGCGCACCTGT 908
901 GCTGCTGAGAGTGCATGACAGCTGAGGAGGCTGGGCGTCCCTCTCTCTCCAG 960
909 GCTGCTGAGAGTGCATGACAGCTGAGGAGGCTGGGCGTCCCTCTCTCTCCAG 968

961 TCTCTAGGCGCTGCTGATGAGAGGCTCCCAAGGGGTTTCAGTCTGACCTATACAGGG 1020
969 TCTCTAGGCGCTGCTGATGAGAGGCTCCCAAGGGGTTTCAGTCTGACCTATACAGGG 1028
1021 AGGCCAAGAGGCGCTCCATGCACTGGAATGC-GGAGCTGCAAGTGTGATTAACCAAGCTC 1079
1029 AGGCCAAGAGGCGCTCCATGCACTGGAATGC-GGAGCTGCAAGTGTGATTAACCAAGCTC 1088
1080 AGGCTTAACAGTACCTCTCTAGTTGAGACACACTGAGAGAGGGTTTTGGAGCTGAA 1139
1089 AGGCTTAACAGTACCTCTCTAGTTGAGACACACTGAGAGAGGGTTTTGGAGCTGAA 1148
1140 TAACTCAGTCACTGTTTCCCATCTCTAAGCCCTTAACCTGACAGCTGCTGTTAATGT 1199
1149 TAACTCAGTCACTGTTTCCCATCTCTAAGCCCTTAACCTGACAGCTGCTGTTAATGT 1208
1200 AGCTTTGATGGAGGTTTCTAGATGAACACTCTCCATGAGGATTTGAACATAGAA 1259
1209 AGCTTTGATGGAGGTTTCTAGATGAACACTCTCCATGAGGATTTGAACATAGAA 1268
1260 GTTATTTGATGGAGGAAAGTCTGAGGGGCAACACAGAAACAGGTCCTCAGCCCA 1319
1269 GTTATTTGATGGAGGAAAGTCTGAGGGGCAACACAGAAACAGGTCCTCAGCCCA 1328
1320 CAGCACTGCTTTTGTGATGACACCCCTCTTAACCTTTATCAGAGATGGGCTGTG 1379
1329 CAGCACTGCTTTTGTGATGACACCCCTCTTAACCTTTATCAGAGATGGGCTGTG 1388
1380 GTCTTGTGTTGCCATCAGACAGACACAGGCACTTAAATATTTAACTTATTTAA 1439
1389 GTCTTGTGTTGCCATCAGACAGACACAGGCACTTAAATATTTAACTTATTTAA 1448
1440 AAGTGAAGAGGATTCATGCTGATGCTTTCTGTGTTGGTGTCTAATATTTGGTGAAGTG 1499
1449 AAGTGAAGAGGATTCATGCTGATGCTTTCTGTGTTGGTGTCTAATATTTGGTGAAGTG 1508
1500 GGGGATCCCAACATCAGGTCCTCCAGATAGCTGTGATGGGCTGATCCAG 1559
1509 GGGGATCCCAACATCAGGTCCTCCAGATAGCTGTGATGGGCTGATCCAG 1568
1560 ATCTTCTTCTCTGGGCTGCTGAGCCGCCCAAAATGCTTAAACCAAGACCTTGAATTTCTA 1619
1569 ATCTTCTTCTCTGGGCTGCTGAGCCGCCCAAAATGCTTAAACCAAGACCTTGAATTTCTA 1628
1620 CTCAATCCCAATGATTAATCCAAATGCTGTACCAAGGTTAGGGTGTGAAGAGTGA 1679
1629 CTCAATCCCAATGATTAATCCAAATGCTGTACCAAGGTTAGGGTGTGAAGAGTGA 1688
1680 GAGGGTGGGCGCTTCAAGGCTCAACGCGCTTCCCTAACACCCCTCTCTTGGCCAGGC 1739
1689 GAGGGTGGGCGCTTCAAGGCTCAACGCGCTTCCCTAACACCCCTCTCTTGGCCAGGC 1748
1740 TGGTTCCTCCCACTTCACTCCCTCTTACTCTCTCTAGGACTGGGCTGATGAAGGACTG 1799
1749 TGGTTCCTCCCACTTCACTCCCTCTTACTCTCTCTAGGACTGGGCTGATGAAGGACTG 1808
1800 CCAAAATTTCCCTTACCCCACTTCCCTTACCCCACTTCCCACTTCCCACTTCCCA 1859
1809 CCAAAATTTCCCTTACCCCACTTCCCTTACCCCACTTCCCACTTCCCACTTCCCA 1868
1860 ACCCTGTTGAGGCTACAGGCTCAAGAGCAAGAGCAAAAGGCGGTTTCCCAAGCTTGTGC 1919
1869 ACCCTGTTGAGGCTACAGGCTCAAGAGCAAGAGCAAAAGGCGGTTTCCCAAGCTTGTGC 1928
1920 CATCTCAGCCCCCAAGTATATCTGTGTTGGGATCTCACAGAACTCAGAGGAC 1979
1929 CATCTCAGCCCCCAAGTATATCTGTGTTGGGATCTCACAGAACTCAGAGGAC 1988
1980 CCCCTGCTGAGCTAAGGAGGCTTATCTCTCAGGGGGGTTTAAAGTCCGTTGCAAT 2039
1989 CCCCTGCTGAGCTAAGGAGGCTTATCTCTCAGGGGGGTTTAAAGTCCGTTGCAAT 2048
2040 AATGTCGTTATTTTAAAGGGGTTGAATTTTATATCTGTAAAGTGAATCAGACT 2099

Dn	2049	AATGCGCTTATTATTATTACGGGGCTGAATTTTATTAACGTAGCTAAGTACATCAAGCT	2108
Oy	2100	ATAATGTTTATGTCACAATAATTAAAGCCTTCTTATATGTTTA	2143
Dn	2109	ATAATGTTTATGTCACAATAATTAAAGCCTTCTTATATGTTTA	2152
RESULT 3			
LOCUS	BC050416	3306 bp	mRNA linear PRI 30-JUN-2004
DEFINITION	Homo sapiens protein protein, mRNA (CDNA clone MGC:54090		
VERSION	IMAGE:0198823), complete cds.		
KEYWORDS	BC050416.2 GI:34194585		
SOURCE	MGC.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
	1 (baaes 1 to 3306)		
	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,		
	Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,		
	Altschul,S.F., Zeeberg,B., Buetow,K.H., Schnefer,C.F., Bhat,N.K.,		
	Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heide,F.,		
	Ditschenko,L., Marinsin,K., Farmer,A.A., Rubin,G.M., Hong,L.,		
	Stapleton,M., Soares,M.B., Bonaldo,W.F., Casavant,T.L.,		
	Scheeet,T.E., Brownstein,M.J., Ueda,T.B., Toshituki,S.,		
	Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,		
	Abrahamson,R.D., Mullaly,S.U., Bosak,S.A., McEwan,P.J.,		
	McKernan,R.D., Malek,J.A., Gunaratne,P.H., Richards,S.,		
	Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hilyk,S.W.,		
	Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,		
	Faley,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,		
	Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,		
	Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D.,		
	Dickson M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,		
	Butterfield,Y.S., Krzywnicki,M.T., Skalka,U., Smalls,D.E.,		
	Scherer,A., Schein,J.E., Jones,S.J., and Merritt,M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length		
JOURNAL	human and mouse cDNA sequences		
PUBMED	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
REFERENCE	12477932		
AUTHORS	2 (baaes 1 to 3306)		
TITLE	Strausberg,R.		
JOURNAL	Direct Submission		
COMMENT	Submitted (08-APR-2003) National Institutes of Health, Mammalian		
	Gene Collection (MGC), Cancer Genomics Office, National Cancer		
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,		
	USA		
	NIH-MGC Project URL: http://mgc.nci.nih.gov		
	On Aug 25, 2003 this sequence version replaced gi:29791944.		
	Contact: MGC help desk		
	Email: gcgabs-remail.nih.gov		
	Tissue Procurement: Dr. James R. Lupski:		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Sequencing Group at the Stanford Human Genome		
	Center, Stanford University School of Medicine, Stanford, CA 94305		
	Web site: http://www.shgc.stanford.edu		
	Contact: (Dickson,Mark) mcdexaxll@stanford.edu		
	R. Dickson, W., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,		
	J.		
FEATURES	Clone distribution: MGC clone distribution information can be found		
	through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov		
	Series: IRAK Plate: 98 Row: n Column: 14		
	This clone was selected for full length sequencing because it		
	passed the following selection criteria: matched mRNA gi: 14916436.		
	Location/Qualifiers		
	1..3306		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
SOURCE			

	/db xref="taxon:9606"	
	/clisue="MGC:54030 IMAGE:6198823"	
	/clisue_type="Peripheral Nervous System, sympathetic trunk"	
	/clone_id="Jupaki_sym pathetic_trunk"	
	/lab_host="DH10B"	
	/note="Vector: pCMV-Sport6"	
	1..3306	
	/gene="Protein"	
	/note="Synonym: PRSt"	
	/db_xref="MIM:608319"	
	248..1909	
CDS	/gene="Protein"	
	/codon_start=1	
	/product="proteine protein"	
	/protein_id="AAH50416.1"	
	/db_xref="GI:29791945"	
	/db_xref="LocustID:85414"	
	/db_xref="MIM:608319"	
	/translaction="MVORLWVSRLRHRKQILLNLITGLSEVCLAAITTYPPILL EVEGEKEMTWLVIGIVGLVCVPLIGSSSDMRGVRPRPTVALSGILISTEL IPRAGMTLAGLCDPDRPLEALILIGGLIDFCGOVCFPLEMLSPFDRPHCRDA YSYAFMIISGGCIGYLPIAIDMDTSLAAYLGTOECLEGLTLIPLTCVAATILVA ERAIQETEPAREGISAPSISSPHCCPCRARLPFNIGLRHLQICCRMRTLRPLFI AEICSMWALMTPLFLTPDIFYBSGLYGCVPARBEGTBARRRDGVNRSGLPLQCI SLVLSVMDLVDFGTFRAYVLASVAAPVPAACATLISHVAAVTAALITGFSL QILLPEPTLASLYHKOKVLFPKRYGDVGASSEDLSMTSFLPGPPLGPFNGHVAGGS GILLPEPTLASGADSVRVVVVGEFTBARVVPNGICIIDLILPSAFPILLSVAPSL FMSTIVLSQSVAIYMVASAGLGIVAIVPATQVFPKSLAKYSA"	
ORIGIN		
Query Match	91.9%; Score 1970; DB 9; Length 3306;	
Best Local Similarity	99.9%; Pred. No. 0;	
Matches 2140; Conservative	0; Mismatches 1; Indels 1; Gaps 1;	
Qy	1 ACCAGGGCGGCCGACGCTGAGCGGGGCAACGAGCGCGGAGACAATTATGATAAGGCG 60	
Db	1149 ACCAGGGCGGCCGACGCTGAGCGGGGCAACGAGCGCGGAGACTATGATAAGAAGCG 1208	
Qy	61 TTCCGAATGGGACAGCTTGAGGCGCTGTTCTCGAGTAGCGCATCTCCCTGGCTCTCTCTGG 120	
Db	1209 TTCCGAATGGGACAGCTTGAGGCGCTGTTCTCGAGTAGCGCATCTCCCTGGCTCTCTCTGG 1268	
Qy	121 TCATGACCGGCTGTGTGTGACGATTTGGGCACTCGAGCAGTCTATTGGCCAAGTGTGCAG 180	
Db	1269 TCATGACCGGCTGTGTGTGACGATTTGGGCACTCGAGCAGTCTATTGGCCAAGTGTGCAG 1328	
Qy	181 CTTTTCCCTGTGGCTGCGCGGTGCCACANAGCCGTGCCCACTAGTGGCCGTGTGACACTT 240	
Db	1329 CTTTTCCCTGTGGCTGCGCGGTGCCCAANAGCCGTGCCCACTAGTGGCCGTGTGACACTT 1388	
Qy	241 CAGCGGCGCTCACCGGAGTTCACTTCTCAACCCTGACGATCTGCCTCTACACACTGGGCT 300	
Db	1389 CAGCGGCGCTCACCGGAGTTCACTTCTCAACCCTGACGATCTGCCTCTACACACTGGGCT 1448	
Qy	301 CCTCTTACCAACCGGAGAACAGAGTGTCTCTGCCAAATACCGAGGGGACACTGGAAGTGTG 360	
Db	1449 CCTCTTACCAACCGGAGAACAGAGTGTCTCTGCCAAATACCGAGGGGACACTGGAAGTGTG 1508	
Qy	361 CTAGCACTGAGGACAGCCTTATGACACGACTTCTGTCCAGAGCCCTTAAGCCTTGAGACTCCCT 420	
Db	1509 CTAGCACTGAGGACAGCCTTATGACACGACTTCTGTCCAGAGCCCTTAAGCCTTGAGACTCCCT 1568	
Qy	421 TCCCTTAATGACACGATGGGTGTGAGAGGACAGTGGCCGTGCCCACTTCCACCCGCGCTCT 480	
Db	1569 TCCCTTAATGACACGATGGGTGTGAGAGGACAGTGGCCGTGCCCACTTCCACCCGCGCTCT 1628	
Qy	481 GCGGGCGCTTGCCTGTGATGTCTCCGTAAGTGTGATGTGGGTGAGCCACCGAGGACCA 540	
Db	1629 GCGGGCGCTTGCCTGTGATGTCTCCGTAAGTGTGATGTGGGTGAGCCACCGAGGACCA 1688	
Qy	541 GGAGTGTTCGGGCGCGGAGCATCTGCGCTGGAACCTCGCCATCTCGAATAGTGACCTTTCCTGC 600	

```

Db      1689 GGGGTGTTCCGGGCGGGGCACTGCTGGACCTCCGCATCTCGATAGTGGCTTCTGCG 1748
Qy      601 TGTCCAGGTGGCCCATCCCTGTTTATGAGGCTCATATGTCAGCTCAGCCAGTGTGCA 660
Db      1749 TGTCCAGGTGGCCCATCCCTGTTTATGAGGCTCATATGTCAGCTCAGCCAGTGTGCA 1808
Qy      661 CTGGCTATATGGGTCTGGCGGAGGCTGGTCTGGTCCCATTTTACTTTTGTACACAG 720
Db      1809 CTGGCTATATGGGTCTGGCGGAGGCTGGTCTGGTCCCATTTTACTTTTGTACACAG 1868
Qy      721 TAGTATTTGACAGAGCGACTTGGCCAAATACACAGTGAAGAACTTGCAGACATTGG 780
Db      1869 TAGTATTTGACAGAGCGACTTGGCCAAATACACAGTGAAGAACTTGCAGACATTGG 1928
Qy      781 GGTGAGGGGCTGCTCACTAGGTCCAGCTCCCGCTCTGTTAGCCCCCATGGGGCTGC 840
Db      1929 GGTGAGGGGCTGCTCACTAGGTCCAGCTCCCGCTCTGTTAGCCCCCATGGGGCTGC 1988
Qy      841 GGGGCTGGCGCGCATGTTCTGTGTCTGCCAAAGTATGTGGCTCTGCTGCCACCTGT 900
Db      1989 GGGGCTGGCGCGCATGTTCTGTGTCTGCCAAAGTATGTGGCTCTGCTGCCACCTGT 2048
Qy      901 GGTGCTGAGGTGCTGATGCTGACAGCTGGGGGCTGGGGGCTCCCTCTCTCTCTCCCGAG 960
Db      2049 GGTGCTGAGGTGCTGATGCTGACAGCTGGGGGCTGGGGGCTCCCTCTCTCTCTCCCGAG 2108
Qy      961 TGTCTAAGGCTGCTGATGCTGAGAGGCTTCCAAAGGGGTTTCACTGATGACATTACAGG 1020
Db      2109 TGTCTAAGGCTGCTGATGCTGAGAGGCTTCCAAAGGGGTTTCACTGATGACATTACAGG 2168
Qy      1021 AGGCGAAGAGGCTCCATGCACTGGAATGC -GGGATCTGCGAGGTGATTAACCCAGGCTGC 1079
Db      2169 AGGCGAAGAGGCTCCATGCACTGGAATGC -GGGATCTGCGAGGTGATTAACCCAGGCTGC 2228
Qy      1080 AGGCTTAACAGCTAGGCTCTCTAGTTGAGACACACTAGAGAAAGGTTTGGAGCTGAA 1139
Db      2229 AGGCTTAACAGCTAGGCTCTCTAGTTGAGACACACTAGAGAAAGGTTTGGAGCTGAA 2288
Qy      1140 TAAACTCAGTCACTGTGTTTCCCATCTGTAAGCCCTTAACTGACGCTTCTGTTAATGT 1199
Db      2289 TAAACTCAGTCACTGTGTTTCCCATCTGTAAGCCCTTAACTGACGCTTCTGTTAATGT 2348
Qy      1200 AGCTCTGATGGAGTTTCTAGAGTGAAGAACTCTCCATGGGATTTGAACATATGAA 1259
Db      2349 AGCTCTGATGGAGTTTCTAGAGTGAAGAACTCTCCATGGGATTTGAACATATGAA 2408
Qy      1260 GTTATTTGAGGGAGAGTCTCTGAGAGGGCAACACAGAAACAGAGTCCCTCAGCCCA 1319
Db      2409 GTTATTTGAGGGAGAGTCTCTGAGAGGGCAACACAGAAACAGAGTCCCTCAGCCCA 2468
Qy      1320 CAGCAGTGTCTTTTGTGCTGATCCACCCCTCTTACCTTTTACAGAGATGGGCTGTG 1379
Db      2469 CAGCAGTGTCTTTTGTGCTGATCCACCCCTCTTACCTTTTACAGAGATGGGCTGTG 2528
Qy      1380 GTTCCTTGTGTCATCAAGAGACAGAGCACTTTAAATTTAATTATTTTAA 1439
Db      2529 GTTCCTTGTGTCATCAAGAGACAGAGCACTTTAAATTTAATTATTTTAA 2588
Qy      1440 AAGTAGAAGGAGTCACTGCTAGCTTTCTGTGTGTGTCTTAATATTTGGGATGGTG 1499
Db      2589 AAGTAGAAGGAGTCACTGCTAGCTTTCTGTGTGTGTCTTAATATTTGGGATGGTG 2648
Qy      1500 GGGGATCCCAACAATCAGGTCCCTGAGATAGCTGTGATTTGGGCTGATTCAGCA 1559
Db      2649 GGGGATCCCAACAATCAGGTCCCTGAGATAGCTGTGATTTGGGCTGATTCAGCA 2708
Qy      1560 AATCTTCTTCTCTGGGCTGTGGCCCCCAAAATGCTTAACCAAGACCTTGGAAATTTCTA 1619
Db      2709 AATCTTCTTCTCTGGGCTGTGGCCCCCAAAATGCTTAACCAAGACCTTGGAAATTTCTA 2768
Qy      1620 CTCATCCCAATATGATTAATCAAAATGCTTACCCCAAGGTAGGGGTGAAGAAAGTA 1679

```

```

Db      2769 CTCATCCCAATATGATTAATCAAAATGCTTACCCCAAGGTAGGGGTGAAGAAAGTA 2828
Qy      1680 GAGGGTGGGGCTTACAGTCTCAACGGCTTCCCTAACACACCTCTTCTTTGGCCAGCC 1739
Db      2829 GAGGGTGGGGCTTACAGTCTCAACGGCTTCCCTAACACACCTCTTCTTTGGCCAGCC 2888
Qy      1740 TGGTTCCTCCCACTTCCACTCCCTCTACTCTCTGAGAGCTGGGCTGATGAAGGACATG 1799
Db      2889 TGGTTCCTCCCACTTCCACTCCCTCTACTCTCTGAGAGCTGGGCTGATGAAGGACATG 2948
Qy      1800 CCCAAATTTTCCCTACCCCAACTTTCCTTACCCTTCCCACTTCCCACTTCCCACTTCCCA 1859
Db      2949 CCCAAATTTTCCCTACCCCAACTTTCCTTACCCTTCCCACTTCCCACTTCCCACTTCCCA 3008
Qy      1860 ACCCTGTTTGAAGCTACTGACAGACCAAGACCAAAAGTGGGTTTCCCAAGCTTTGTC 1919
Db      3009 ACCCTGTTTGAAGCTACTGACAGACCAAGACCAAAAGTGGGTTTCCCAAGCTTTGTC 3068
Qy      1920 CACTTCAGCCCCCAAGTATCTGTGCTTGGGGAATCTCACAGAACTCAGAGGAC 1979
Db      3069 CACTTCAGCCCCCAAGTATCTGTGCTTGGGGAATCTCACAGAACTCAGAGGAC 3128
Qy      1980 CCCCTGCTGAGCTAAGGAGGCTTATCTCAAGGGGGTTTAAAGTCCGTTTGCAT 2039
Db      3129 CCCCTGCTGAGCTAAGGAGGCTTATCTCAAGGGGGTTTAAAGTCCGTTTGCAT 3188
Qy      2040 AATGTGCTTATTTTATTTTATGCGGGGTGAATTTTATCTGTAAGTGAATCAGAGT 2099
Db      3189 AATGTGCTTATTTTATTTTATGCGGGGTGAATTTTATCTGTAAGTGAATCAGAGT 3248
Qy      2100 AATATGTTTATGTCACAAATTTAAAGCTTCTTATATGTT 2141
Db      3249 AATATGTTTATGTCACAAATTTAAAGCTTCTTATATGTT 3290

RESULT 4
AR278710
LOCUS AR278710 2904 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 703 from patent US 6512094.
ACCESSION AR278710
VERSION AR278710.1 GI:29712956
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 2904)
XU,J., DILLON,D.C., MITCHAM,J.L., HARLOCKER,S.L., JIANG,X.,
KALOS,M.D., FANGER,G.R., RETTER,M.W., STOLK,J.A., DAY,C.H.,
VEDDICK,T.S., CARTER,D., LI,S.X., WANG,A., SKELLY,Y.A.W.,
HEPLER,W.T. and HENDERSON,R.A.
Compositions and methods for the therapy and diagnosis of prostate
cancer
Patent: US 6512094-A 703 28-JAN-2003;
JOURNAL Location/Qualifiers
FEATURES
1..2904
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 89.4%; Score 1916; DB 6; Length 2904;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2086; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Qy 57 GGCCTTGGAGGGGAGCCTGGGGGCTGTTCTGCAAGTGGGCATCTCCGTGCTTCTCT 116
Db 813 GGCCTTGGAGTGGGAGCCTGGGGGCTGTTCTGCAAGTGGGCATCTCCGTGCTTCTCT 872
Qy 117 CTGGTCATGAGACCGGCTGGTGTGAGGATTCGGCACTCGAGCAGTCTATTTGGCAGTGTG 176
Db 873 CTGGTCATGAGACCGGCTGGTGTGAGGATTCGGCACTCGAGCAGTCTATTTGGCAGTGTG 932
Qy 177 GCAGCTTCCCTGTGGCTGCGGGTGCACATGCTGTCCACAGTGTGCGGTGATGACA 236

```

Db 933 GCAGCTTTCCTGTGGCTGCCGGTGCACATGCTGTCCACAGTGTGGCCGTGTGACA 992
Qy 237 GCTTCAGCGCGCCCTCACCGGGTTTCACTTCTCAAGCTTGCAGATCTGCTCCCTACACACTG 296
Db 993 GCTTCAGCGCGCCCTCACCGGGTTTCACTTCTCAAGCTTGCAGATCTGCTCCCTACACACTG 1052
Qy 297 GCTTCCTCTTACACCGGGAGAAAGCAGGTGTCTGCGCCAAATACCGAGGGGACACTGGA 356
Db 1053 GCTTCCTCTTACACCGGGAGAAAGCAGGTGTCTGCGCCAAATACCGAGGGGACACTGGA 1112
Qy 357 GGTGTCTGACGTAGGACAGCTGTATACCACTTCTGCGCAGGCTTAAAGCTGTGAGCT 416
Db 1113 GGTGTCTGACGTAGGACAGCTGTATACCACTTCTGCGCAGGCTTAAAGCTGTGAGCT 1172
Qy 417 CCTTTCCTTATGAGACAGTGGGTGTGAGGACAGTGGCTTCCCACTTCCACCGCG 476
Db 1173 CCTTTCCTTATGAGACAGTGGGTGTGAGGACAGTGGCTTCCCACTTCCACCGCG 1232
Qy 477 CTGTGCGGGGCTCTGTGCTGTGATGTCTCCGTACGTGTGGTGGGTGAGCCACGAG 536
Db 1233 CTGTGCGGGGCTCTGTGCTGTGATGTCTCCGTACGTGTGGTGGGTGAGCCACGAG 1292
Qy 537 GCCAGGGTGGTTCGGGCGCGGGGCAATGTGCTGGAAGCTGCGCAATCTGTGATAGTGCCTTC 596
Db 1293 GCCAGGGTGGTTCGGGCGCGGGGCAATGTGCTGGAAGCTGCGCAATCTGTGATAGTGCCTTC 1352
Qy 597 CTGCTGTCCAGAGTGGCCCATCCCTGTTTATGAGGCTTCAATGTCACAGCTACGCCAGTCT 656
Db 1353 CTGCTGTCCAGAGTGGCCCATCCCTGTTTATGAGGCTTCAATGTCACAGCTACGCCAGTCT 1412
Qy 657 GTCACTGCTTATATGTGTCTGTGCGGACAGGCTTGGTGTGCGCCATTTACTTTGTGTACA 716
Db 1413 GTCACTGCTTATATGTGTGTGTGCGGACAGGCTTGGTGTGCGCCATTTACTTTGTGTACA 1472
Qy 717 CAGGTATATTTTACAAAGAGCGACTTGGCCAAATACTCAAGCTTGAAGAACTTCCAGACA 776
Db 1473 CAGGTATATTTTACAAAGAGCGACTTGGCCAAATACTCAAGCTTGAAGAACTTCCAGACA 1532
Qy 777 TTGGGGTGAAGGGCTGTGCTCACTGGGTCCAGCTCCCGCTCTGTATGACCCTAAGGGG 836
Db 1533 TTGGGGTGAAGGGCTGTGCTCACTGGGTCCAGCTCCCGCTCTGTATGACCCTAAGGGG 1592
Qy 837 CTGCGCGGGCTGTGCGCGCACTTCTGTGCTGCCAAATATGTGCTCTGTGCTGCCAC 896
Db 1593 CTGCGCGGGCTGTGCGCGCACTTCTGTGCTGCCAAATATGTGCTCTGTGCTGCCAC 1652
Qy 897 CTGTGCTGCTGAGTGTGCTGAGCTGACAGCTGAGGGGCTGGGGGCTGCTCTCTCTCC 956
Db 1653 CTGTGCTGCTGAGTGTGCTGAGCTGACAGCTGAGGGGCTGGGGGCTGCTCTCTCTCC 1712
Qy 957 CCAGTCTTAGGGGCTGCTGACTGAGAGGCTTCCAAAGGGGTTTCAAGTCTGACTTTATAC 1016
Db 1713 CCAGTCTTAGGGGCTGCTGACTGAGAGGCTTCCAAAGGGGTTTCAAGTCTGACTTTATAC 1772
Qy 1017 AGGGAGGCGCAGAAAGGGCTCAGCACTGGAATGC-GGAACTCTGCAAGTGTGATTCAG 1075
Db 1773 AGGGAGGCGCAGAAAGGGCTCAGCACTGGAATGC-GGAACTCTGCAAGTGTGATTCAG 1832
Qy 1076 GCTCAAGGGTTAAACAGTACGCTCTAGTTGAGACACACTAGAGAAAGGTTTGGAGAC 1135
Db 1833 GCTCAAGGGTTAAACAGTACGCTCTAGTTGAGACACACTAGAGAAAGGTTTGGAGAC 1892
Qy 1136 TGAATTAACCTCAGTCACTGCTGTTTCCATCTCTAAAGCCCTTAACTCAGCTTGTTA 1195
Db 1893 TGAATTAACCTCAGTCACTGCTGTTTCCATCTCTAAAGCCCTTAACTCAGCTTGTTA 1952
Qy 1196 ATGTAGCTCTTGCATGGGAGTTTCTAAGATGAACACCTCCATGGGATTTGAACATAT 1255
Db 1953 ATGTAGCTCTTGCATGGGAGTTTCTAAGATGAACACCTCCATGGGATTTGAACATAT 2012
Qy 1256 GAAAGTTATTTGTAGGGGAAAGTCTGAGGGGCAACACAAAGAACAGGTTCCCTCAG 1315
Db 2013 GAAAGTTATTTGTAGGGGAAAGTCTGAGGGGCAACACAAAGAACAGGTTCCCTCAG 2072

Qy 1316 CCCACAGCACTGTCTTTTGTGTGATCCACCCCTCTTACCTTTATCAGATGTGGCT 1375
Db 2073 CCCACAGCACTGTCTTTTGTGTGATCCACCCCTCTTACCTTTATCAGATGTGGCT 2132
Qy 1376 GTTGTGCTCTTGTGTGCTCATCAGAGACACAGGATTTAAATTTATTTATTT 1435
Db 2133 GTTGTGCTCTTGTGTGCTCATCAGAGACACAGGATTTAAATTTATTTATTT 2192
Qy 1436 AACAAAGTGAAGGAAATCCATTTGTAGCTTTTGTGTGTGTGTCTAATATTTGGTAG 1495
Db 2193 AACAAAGTGAAGGAAATCCATTTGTAGCTTTTGTGTGTGTGTCTAATATTTGGTAG 2252
Qy 1496 GGTGGGGATCCCAACATCAGTCCCTGAGATAGTGTCTATTTGGCTGATCTTGC 1555
Db 2253 GGTGGGGATCCCAACATCAGTCCCTGAGATAGTGTCTATTTGGCTGATCTTGC 2312
Qy 1556 CAGAAATCTTCTCTGTGGGGTGTGGGCCCCCAAAATGCCCTAACCCAGACCTTGGAAAT 1615
Db 2313 CAGAAATCTTCTCTGTGGGGTGTGGGCCCCCAAAATGCCCTAACCCAGACCTTGGAAAT 2372
Qy 1616 TCTACTCATCCCAATGATTAATTCCAATGCTGTACCCAAAGTTAGGGTGTGAAGAA 1675
Db 2373 TCTACTCATCCCAATGATTAATTCCAATGCTGTACCCAAAGTTAGGGTGTGAAGAA 2432
Qy 1676 GGTAAAGGTGGGCTTCAAGTCTCAGGCTTCCCTAACCAACCCCTCTCTTGGGCC 1735
Db 2433 GGTAAAGGTGGGCTTCAAGTCTCAGGCTTCCCTAACCAACCCCTCTCTTGGGCC 2492
Qy 1736 AGCTGTGTCCCCCACTTCCCTCACTCCCTCACTCTGTAGGACTGGGCTGATGAAGGC 1795
Db 2493 AGCTGTGTCCCCCACTTCCCTCACTCCCTCACTCTGTAGGACTGGGCTGATGAAGGC 2552
Qy 1796 ACTGCCAAATTTTCCCTCACTCCCTCACTTCCCTCACTTCCCTCACTTCCCTCACT 1855
Db 2553 ACTGCCAAATTTTCCCTCACTCCCTCACTTCCCTCACTTCCCTCACTTCCCTCACT 2612
Qy 1856 CACAAACCTGTGTGAGCTACTGAGAGACAGAAAGCAACAAAGTGGTGTTCACAGCTT 1915
Db 2613 CACAAACCTGTGTGAGCTACTGAGAGACAGAAAGCAACAAAGTGGTGTTCACAGCTT 2672
Qy 1916 TGTTCATCTCAGCCCGCAGATATCTGTGTGGGAAATCTCACAAGAACTCAGGA 1975
Db 2673 TGTTCATCTCAGCCCGCAGATATCTGTGTGGGAAATCTCACAAGAACTCAGGA 2732
Qy 1976 GCACCCCTGTGCTGAGTAAAGGAGTCTTATCTCTCAGGGGGGTTAAAGTCCGTTTG 2035
Db 2733 GCACCCCTGTGCTGAGTAAAGGAGTCTTATCTCTCAGGGGGGTTAAAGTCCGTTTG 2792
Qy 2036 CAATATGTGCTTATTTTATAGGGGGTGAATATTTATCTGAAGTGAAGCAATCA 2095
Db 2793 CAATATGTGCTTATTTTATAGGGGGTGAATATTTATCTGAAGTGAAGCAATCA 2852
Qy 2096 GAGTATATGTTATGTGTGAACAAATTTAAAGGCTTCTTATATGTTTA 2143
Db 2853 GAGTATATGTTATGTGTGAACAAATTTAAAGGCTTCTTATATGTTTA 2900

RESULT 5
AR400442
LOCUS AR400442 2904 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 703 from patent US 6620922.
ACCESSION AR400442
VERSION AR400442.1 GI:40143818
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2904)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kolos,M.D., Fargel,G.R., Reiter,W.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.

TITLE	Compositions and methods for the therapy and diagnosis of prostate Cancer
JOURNAL	Patent: US 6620922-A 703 16-SEP-2003;
FEATURES	Location/Qualifiers
SOURCE	1..2904
ORIGIN	/Organisms="unknown" /mol_type="genomic DNA"

Query Match	89.4%	Score 1916	DB 6	length 2904
Best Local Similarity	99.9%	Pred. No. 0		
Matches 2086	Conservative	0	Mismatches 1	Indels 1

QY	57	GGCGTTGGGATGAGGAGCGCTGGGGGCGTGTTCCTGACAGTGGCGCAATCCCTCGGTCTTCTCT	116
Db	813	GGCGTTGGGATGAGGAGCGCTGGGGGCGTGTTCCTGACAGTGGCGCAATCCCTCGGTCTTCTCT	872
QY	117	CTGTGATGAGACCGGCTGTGTGACGGAATTCGCACTCGACAGTCTAATTGGACAGTGTG	176
Db	873	CTGTGATGAGACCGGCTGTGTGACGGAATTCGCACTCGACAGTCTAATTGGACAGTGTG	932
QY	177	GCAGCTTTCCTGTGTGGCTGTCCGGGTGCGACAATCCCTGTCCCAAGTGTGGCCGTGGTGACA	236
Db	933	GCAGCTTTCCTGTGTGGCTGTCCGGGTGCGACAATCCCTGTCCCAAGTGTGGCCGTGGTGACA	992
QY	237	GCTTCAGCGCGCCCTGACCGGGGTTCACCTTCTCAGCCCTTGACAGATCTTGCCCTACACACTG	296
Db	993	GCTTCAGCGCGCCCTGACCGGGGTTCACCTTCTCAGCCCTTGACAGATCTTGCCCTACACACTG	1052
QY	297	GCTTCCTCTTACACCGGGAGAGACAGGTGTTCCTGTCCCAATTCGAGGGGACACTGGA	356
Db	1053	GCTTCCTCTTACACCGGGAGAGACAGGTGTTCCTGTCCCAATTCGAGGGGACACTGGA	1112
QY	357	GGTGTACAGTGAAGAGACCGCTGATGACACAGCTTCTGTGCGACGGCCCTTAAGCTGTGAGGT	416
Db	1113	GGTGTACAGTGAAGAGACCGCTGATGACACAGCTTCTGTGCGACGGCCCTTAAGCTGTGAGGT	1172
QY	417	CCCTTCCCTAATGACACAGTGGGTCTGGAAGGCAAGTGGCTGTCCACCTTCACCCGG	476
Db	1173	CCCTTCCCTAATGACACAGTGGGTCTGGAAGGCAAGTGGCTGTCCACCTTCACCCGG	1232
QY	477	CTGTGCGGGGGCTCTGTGTAATGTCTCCGTAAGTGTGTGTGGGTGAGCCCAACCGAG	536
Db	1233	CTGTGCGGGGGCTCTGTGTAATGTCTCCGTAAGTGTGTGTGGGTGAGCCCAACCGAG	1292
QY	537	GCCAGAGGTGTTCGCGGCGCGGGGACATGTGCGACCTTCGCATCTTGGAATGATGACTTTC	596
Db	1293	GCCAGAGGTGTTCGCGGCGCGGGGACATGTGCGACCTTCGCATCTTGGAATGATGACTTTC	1352
QY	597	CTGTGTCTCCAGGTGGCCCATCCTGTTTAATGGGCTCCATTTGTCCAGCTCAGCCAGTCT	656
Db	1353	CTGTGTCTCCAGGTGGCCCATCCTGTTTAATGGGCTCCATTTGTCCAGCTCAGCCAGTCT	1412
QY	657	GTCACGTGCTATATATGTGTCTGCGCAGAGGCTGGGTGTGGTGGCAATTACTTGTCTACA	716
Db	1413	GTCACGTGCTATATATGTGTCTGCGCAGAGGCTGGGTGTGGTGGCAATTACTTGTCTACA	1472
QY	717	CAGGTAGTATTGACAAAGACGACTTGGCCAAATATCTACGCTAGAAAACTTCGACACA	776
Db	1473	CAGGTAGTATTGACAAAGACGACTTGGCCAAATATCTACGCTAGAAAACTTCGACACA	1532
QY	777	TTGGGGTGAAGGCGCTGTGCTCACTGAGGTCCAGGCTCCCGCTCTGTTAAGCCCAATGGGG	836
Db	1533	TTGGGGTGAAGGCGCTGTGCTCACTGAGGTCCAGGCTCCCGCTCTGTTAAGCCCAATGGGG	1592
QY	837	CTGCAGGAGCTGGCCGCGCAATTTCTGTGTGCTGTGCCAAAGTATGTGCTCTCTGCTCCAC	896
Db	1593	CTGCAGGAGCTGGCCGCGCAATTTCTGTGTGCTGTGCCAAAGTATGTGCTCTCTGCTCCAC	1652
QY	897	CTGTGTCTGTAGAGTGTGCGTAGCTGACACAGTGTGGGGCTGGGGCGTTCCTCTCTCTCTCC	956
Db	1653	CTGTGTCTGTAGAGTGTGCGTAGCTGACACAGTGTGGGGCTGGGGCGTTCCTCTCTCTCTCC	1712

QY	957	COAGTCTCTAAGGGCTGCTGACTGAGAGGCTTCCAAAGGGGTTCAGTCTGAGACTTAAC	1016
Db	1713	CCAGCTCTTAAGGGCTGCTGACTGAGAGGCTTCCAAAGGGGTTCAGTCTGAGACTTAAC	1772
QY	1017	AGGAGGCGCAAAAGGGCTCCATGCACTGGAATGC -GGGACTCTGCAGTGATTAACCAAG	1075
Db	1773	AGGAGGCGCAAAAGGGCTCCCAATGCACTGGAATGCGGGGACTCTGCAAGTGTATTAACCAAG	1832
QY	1076	GCTCAGGGGTTAACAGCTAGCCTCTAGTGTGAGACACACTAGAAAGAGGTTTTGGAGAGC	1135
Db	1833	GCTCAGGGGTTAACAGCTAGCCTCTAGTGTGAGACACACTAGAGAGAGGTTTTGGAGAGC	1892
QY	1136	TGAATAAACTCAGTCACTGGTATTCATCTCTAAGCCCTTAACTGCAAGCTTCGTTTTA	1195
Db	1893	TGAATAAACTCAGTCACTGGTATTCATCTCTAAGCCCTTAACTGCAAGCTTCGTTTTA	1952
QY	1196	ATGTATGCTCTTGCAATGGAGAGTTTCTTAGATGAACACTCTCTCCATGGGATTTGAACATAT	1255
Db	1953	ATGTATGCTCTTGCAATGGAGAGTTTCTTAGATGAACACTCTCTCCATGGGATTTGAACATAT	2012
QY	1256	GAAAGTTATTTGTAGGGGAAGTCTGTAAGGGGCAACACAAAGACAGAGTCCCTCAG	1315
Db	2013	GAAAGTTATTTGTAGGGGAAGTCTGTAAGGGGCAACACAAAGACAGAGTCCCTCAG	2072
QY	1316	CCCAACAGCACTGTCTTTTGTGCTGATCCACCCCTCTTACTCTTTTATCAGAGTGTGCT	1375
Db	2073	CCCAACAGCACTGTCTTTTGTGCTGATCCACCCCTCTTACTCTTTTATCAGAGTGTGCT	2132
QY	1376	GTTGTGCTCTTCTGTGGCCATCAACAGACACAGGCAATTTAATATTTAATCTTATTTT	1435
Db	2133	GTTGTGCTCTTCTGTGGCCATCAACAGACACAGGCAATTTAATATTTAATCTTATTTT	2192
QY	1436	AACAAAGTAGAAGGAATCCATCTGACTTTTCTGTGTGATGCTTAATATTGGGTAG	1495
Db	2193	AACAAAGTAGAAGGAATCCATCTGACTTTTCTGTGTGATGCTTAATATTGGGTAG	2252
QY	1496	GGTGGGGGATCCCAACATCAGGTCCCTGAGATAGCTGTGCTATTGGGCTGATCATTC	1555
Db	2253	GGTGGGGGATCCCAACATCAGGTCCCTGAGATAGCTGTGCTATTGGGCTGATCATTC	2312
QY	1556	CAGAAATCTTCTTCTCTGAGGGTCTGGGCCCCCAAAATGCTTAACCCAGACCTTGGAAAT	1615
Db	2313	CAGAAATCTTCTTCTCTGAGGGTCTGGGCCCCCAAAATGCTTAACCCAGACCTTGGAAAT	2372
QY	1616	TCTACTATCCCAATGATATTTCCAAATGCTGTTAACCAAGTTTAGGGTGAAGAA	1675
Db	2373	TCTACTATCCCAATGATATTTCCAAATGCTGTTAACCAAGTTTAGGGTGAAGAA	2432
QY	1676	GGTAGAGGGTGGGGCTTCAGGCTCAACAGGCTTCCCTAACACACCCCTTCTCTTGAGCC	1735
Db	2433	GGTAGAGGGTGGGGCTTCAGGCTCAACAGGCTTCCCTAACACACCCCTTCTCTTGAGCC	2492
QY	1736	AGCTGTGTTCCCCCACACTTCACACTCCCCCTACTCTCTAAGGACTGGGCTGATGAAGGC	1795
Db	2493	AGCTGTGTTCCCCCACACTTCACACTCCCCCTACTCTCTAAGGACTGGGCTGATGAAGGC	2552
QY	1796	ACTGGCCAAATTTCCCTTACCCGCAACTTCCGCTACCCCACTTCCCACTGCACTC	1855
Db	2553	ACTGGCCAAATTTCCCTTACCCGCAACTTCCGCTACCCCACTTCCCACTGCACTC	2612
QY	1856	CACAAACCTGTTTGAAGTACTGACAGACCAAGAGCAAAAGTGGGTTTTCCAAAGCTT	1915
Db	2613	CACAAACCTGTTTGAAGTACTGACAGACCAAGAGCAAAAGTGGGTTTTCCAAAGCTT	2672
QY	1916	TGTTCATCTCAGCCCCCAGAGTATATCTGTGCTTGGGAATCTCAACAGAACTCAGGA	1975
Db	2673	TGTTCATCTCAGCCCCCAGAGTATATCTGTGCTTGGGAATCTCAACAGAACTCAGGA	2732
QY	1976	GCACCCCCCTGCTAGGCTAAGGGAGGCTTAATCTCTAGGGGGGGTTTAATGTGCGTTG	2035
Db	2733	GCACCCCCCTGCTAGGCTAAGGGAGGCTTAATCTCTCTAGGGGGGGTTTAATGTGCGTTG	2792
QY	2036	CAATATGTCTCTTATTTTGTGCGGGGTGAATATTTATACTGTATGACATCA	2095

Db 2793 CAATTAAGTGTCTATTATTATTTAGCCGGGTGAATATTTTACTGTAAGTGAACATCA 2852
QY 2096 GAGTATATATGTTTATGTTGACAAATTAAGCTTTCTTATATGTTTA 2143
Db 2853 GAGTATATATGTTTATGTTGACAAATTAAGCTTTCTTATATGTTTA 2900

RESULT 6
AR405709
LOCUS AR405709 2904 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 703 from patent US 6630305.
ACCESSION AR405709
VERSION AR405709.1 GI:40154546
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2904)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kelloff,M.D., Fanger,G.R., Reiter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skelley,Y.A.W., Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate cancer
JOURNAL Patent: US 6630305-A 703 07-OCT-2003;
FEATURES
source 1..2904
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 89.4%; Score 1916; DB 6; Length 2904;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2086; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 57 GGGCTTCGATGGGAGCCCTGGGGCTGTTCTGTCAGTGGCCATCTCCCTGCTCTCT 116
Db 813 GGGGTTGGATGGGAGCCCTGGGGCTGTTCTGTCAGTGGCCATCTCCCTGCTCTCT 872
QY 117 CTGGTATGGAACCGGCTGTGTGCGAGCATTCGAGCATCGAGCATTAATTTGGCAGTGTG 176
Db 873 CTGGTATGGAACCGGCTGTGTGCGAGCATTCGAGCATCGAGCATTAATTTGGCAGTGTG 932
QY 177 GCAAGCTTCCCTGTGCTGCTGCGGTGCGACATGCTCTCCACAGTGTGCGGTGAGACA 236
Db 933 GCAAGCTTCCCTGTGCTGCTGCGGTGCGACATGCTCTCCACAGTGTGCGGTGAGACA 992
QY 237 GCTTACGCCCTCTACCGGGTTCACTTCTCAGCCCTGCAATCTCTGCTTACACACTG 296
Db 993 GCTTACGCCCTCTACCGGGTTCACTTCTCAGCCCTGCAATCTCTGCTTACACACTG 1052
QY 297 GCCTCCCTCTACCAACCGGGAGAAAGAGGTTCCTGCGCAATATCCAGAGGGACACTGGA 356
Db 1053 GCCTCCCTCTACCAACCGGGAGAAAGAGGTTCCTGCGCAATATCCAGAGGGACACTGGA 1112
QY 357 GGTGTAGACAGTGAAGACAGCTGTATGACAGCTTCTCTGCGAGCCCTTAAGCCTGAGCT 416
Db 1113 GGTGTAGACAGTGAAGACAGCTGTATGACAGCTTCTCTGCGAGCCCTTAAGCCTGAGCT 1172
QY 417 CCTTTCCTTAATGAGACAGTGGGTGTGAGAGGAGTGGCTCTCCACTCCACCCGG 476
Db 1173 CCTTTCCTTAATGAGACAGTGGGTGTGAGAGGAGTGGCTCTCCACTCCACCCGG 1232
QY 477 CTCTGGGGGGCTCTGCTGTGATGTCCTGACAGTGGTGGTGGAGGCCACCGAG 536
Db 1233 CTCTGGGGGGCTCTGCTGTGATGTCCTGACAGTGGTGGTGGAGGCCACCGAG 1292
QY 537 GCCAAGGTGTTCCGGGCGGGGCACTGCTGAGACTTGCCACTCTGGATATGCTCTTC 596
Db 1293 GCCAAGGTGTTCCGGGCGGGGCACTGCTGAGACTTGCTGCACTCTGGATATGCTCTTC 1352
QY 597 CTGCTGTCCCAAGTGGCCCAATCCCTGTTTATGGGCTCAATTTGCAAGTCAAGCTCA 656

Db 1353 CTGCTGTCCCAAGTGGCCCAATCCCTGTTTATGGGCTCAATTTGCAAGTCAAGCTCT 1412
QY 657 GTCACTGACCTATATGATGTGTCTGCGCAGGCTCGGGTGTGTCGCAATTAATTTGTGACA 716
Db 1413 GTCACTGACCTATATGATGTGTCTGCGCAGGCTCGGGTGTGTCGCAATTAATTTGTGACA 1472
QY 717 CAGGTATGTTTGAACAGAGCGACTTGGCCAAATATCTAGCGTAGAAAACTTCCAGACACA 776
Db 1473 CAGGTATGTTTGAACAGAGCGACTTGGCCAAATATCTAGCGTAGAAAACTTCCAGACACA 1532
QY 777 TTGGGGTGAAGGCGCTGCTCACTGGGTCCAGTCTCCCGCTCTGTTAGCCCAATGGGG 836
Db 1533 TTGGGGTGAAGGCGCTGCTCACTGGGTCCAGTCTCCCGCTCTGTTAGCCCAATGGGG 1592
QY 837 CTGCGGGCTGACCGCCAGTTTCTGTGCTGTCGCAAGTATATGTGCTCTCTGCCACC 896
Db 1593 CTGCGGGCTGACCGCCAGTTTCTGTGCTGTCGCAAGTATATGTGCTCTCTGCCACC 1652
QY 897 CTGTGCTGTAGAGTGTGCTGAGTGTGACAGCTGTGGGGCTGGGGCTCTCTCTCTTCC 956
Db 1653 CTGTGCTGTAGAGTGTGCTGAGTGTGACAGCTGTGGGGCTGGGGCTCTCTCTCTTCC 1712
QY 957 CCAGTCTCTAAGGGCTGCTGACTGAGAGGCTTCCAAAGGGGGTTTCAGTGTGACTATAC 1016
Db 1713 CCAGTCTCTAAGGGCTGCTGACTGAGAGGCTTCCAAAGGGGGTTTCAGTGTGACTATAC 1772
QY 1017 AGGAGGCCAAGAGGGCTCTCATGCACTGGAATGC-GGGACTCTGCAAGTGAATACCGAG 1075
Db 1773 AGGAGGCCAAGAGGGCTCTCATGCACTGGAATGC-GGGAGGCTCTGCAAGTGAATACCGAG 1832
QY 1076 GCTCAGGGTTAAGCTAGCTGCTCCGATGTTGAGACACACTTGAAGAGGTTTGGAGGC 1135
Db 1833 GCTCAGGGTTAAGCTAGCTGCTCCGATGTTGAGACACACTTGAAGAGGTTTGGAGGC 1892
QY 1136 TGAATTAACAGTCACTGCTTCCATCTCTAAGCCCTTAACTCTCAGCTTCTGTTA 1195
Db 1893 TGAATTAACAGTCACTGCTTCCATCTCTAAGCCCTTAACTCTCAGCTTCTGTTA 1952
QY 1196 ATGTAGCTCTTGCATGGAGGTTTCTAGATGAACACTCTCTCATGGGATTTGAACATAT 1255
Db 1953 ATGTAGCTCTTGCATGGAGGTTTCTAGATGAACACTCTCTCATGGGATTTGAACATAT 2012
QY 1256 GAAAGTTATTTGAGGGAAGTCTGAGGGGGAACAACAAGAACAGTCCCTCAG 1315
Db 2013 GAAAGTTATTTGAGGGAAGTCTGAGGGGGAACAACAAGAACAGTCCCTCAG 2072
QY 1316 CCACAGCACTGTCTTTTGTGATCCACCCCTCTTACCTTTATCAGAGTGTGCT 1375
Db 2073 CCACAGCACTGTCTTTTGTGATCCACCCCTCTTACCTTTATCAGAGTGTGCT 2132
QY 1376 GTTGTCTCTTGTGTCATACAGAGACACAGGACTTTAAATTTTAACTTATTTATTT 1435
Db 2133 GTTGTCTCTTGTGTCATACAGAGACACAGGACTTTAAATTTTAACTTATTTATTT 2192
QY 1436 AACAAAGTAAGAGGAATCCATGCTAGCTTCTGATGGTGGTGAATTTGGGTAG 1495
Db 2193 AACAAAGTAAGAGGAATCCATGCTAGCTTCTGATGGTGGTGAATTTGGGTAG 2252
QY 1496 GGTGGGGATCCCAACATCAGGTCTCCGAGATAGCTGTCAATGGGCTGATCTTGC 1555
Db 2253 GGTGGGGATCCCAACATCAGGTCTCCGAGATAGCTGTCAATGGGCTGATCTTGC 2312
QY 1556 CAGAACTCTTCTCTCGGGGTCTGGGCCCCCAAAAGTCTTACCCAGACCTTGAAT 1615
Db 2313 CAGAACTCTTCTCTCGGGGTCTGGGCCCCCAAAAGTCTTACCCAGACCTTGAAT 2372
QY 1616 TCTACTATCCCAATATATATTCCAATGCTGTATCCCAAGTTAGAGTGTGAAGAA 1675
Db 2373 TCTACTATCCCAATATATATTCCAATGCTGTATCCCAAGTTAGAGTGTGAAGAA 2432
QY 1676 GTTGAAGGTGGGGCTTCAAGTCTCAACGAGCTTCCCTTACCAACCCCTCTTCTTGGGCC 1735

Db	2433	GGTAAAGGGTGGGACCTTAAGGCTTCACAGCGCTTCCCTAACCAACCCTTTCTTTGGGCC	2492
Qy	1736	AGCCGTGATCCCCCACCATTTCACATCCCCTACTCTCTCTAAGCATGGGCTGATGAAGGC	1795
Db	2493	AGCGTGATCCGCCCACTTCCACATCCTCCTACTCTCTCTAAGCATGGGCTGATGAAGGC	2552
Qy	1786	ACTGCCCAAATTTTCCCTCACCCCACTTTCCCTTACCCCAACTTTCCCAACAGCTC	1855
Db	2553	ACTGCCCAAATTTTCCCTCACCCCACTTTCCCTTACCCCAACTTTCCCAACAGCTC	2612
Qy	1856	CACAACCCCTGTTTTGGAGCTACGACGAGACCAAGAACAAGTGGTTTTCCCAAGCTT	1915
Db	2613	CACAACCCCTGTTTTGGAGCTACGACGAGACCAAGAACAAGTGGTTTTCCCAAGCTT	2672
Qy	1916	TGTCATCTCAGACCCCCAGAGATATCTGTGCTTGGGAGATCTCACAAGAACTCAGGA	1975
Db	2673	TGTCATCTCAGACCCCCAGAGATATCTGTGCTTGGGAGATCTCACAAGAACTCAGGA	2732
Qy	1976	GCACCCCTGCTCTAGCTAAGGAGAGTCTTATCTCTCAGGGGGGTTTAAAGTCCGTTTG	2035
Db	2733	GCACCCCTGCTCTAGCTAAGGAGAGTCTTATCTCTCAGGGGGGTTTAAAGTCCGTTTG	2792
Qy	2036	CAATAATGCTGCTTATTTTTTTAGCGGGGGGANAATTTTATCTGTAAGAGCAATCA	2095
Db	2793	CAATAATGCTGCTTATTTTTTTAGCGGGGGGANAATTTTATCTGTAAGAGCAATCA	2852
Qy	2096	GAGTAAATGTTTATGTGACAAAATTAAGGCTTTCTTATATGTTTA	2143
Db	2853	GAGTAAATGTTTATGTGACAAAATTAAGGCTTTCTTATATGTTTA	2900
RESULT 7			
LOCUS	ARS64089	2904 bp	DNA
DEFINITION	Sequence 703 from patent US 6759515.		
ACCESSION	ARS64089		
VERSION	ARS64089.1	GI:53979140	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 2904)		
AUTHORS	Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Khalo,M.D., Fanger,G.R., Reiter,M.W., Stolk,J.A., Day,C.H., Vedlick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A. Compositions and methods for the therapy and diagnosis of prostate cancer Patent: US 6759515-A 703 06-JUL-2004; Location/Qualifiers 1..2904 /organism="unknown" /mol_type="genomic DNA"		
JOURNAL			
FEATURES			
source			
ORIGIN			
Query Match	89.4%	Score 1916;	DB 6; Length 2904;
Best Local Similarity	99.9%	Pred. No. 0;	
Matches 2086;	Conservative 0;	Mismatches 1;	Indels 1; Gaps 1;
Qy	57	GAGCGTTGCGATGGGACGCTTGAGGCTGTTCTCGAGTGGCGCATCTCCCTGATCTTCT	116
Db	813	GAGCGTTGCGAATGGGACGCTTGAGGCTGTTCTCGAGTGGCGCATCTCCCTGATCTTCT	872
Qy	117	CTGGTCATGAGACCGGCTGTGACAGGATTTGGGCACTGAGAGATCTATTGGCAAGTGTG	176
Db	873	CTGGTCATGAGACCGGCTGTGACAGGATTTGGGCACTGAGAGATCTATTGGCAAGTGTG	932
Qy	177	GCAGCTTCCCTGTGGCTGCGGATGCCATAGCTCTGCCACAGTGTGGCGTGGTACA	236
Db	933	GCAGCTTCCCTGTGGCTGCGGATGCCACATAGCTCTGCCACAGTGTGGCGTGGTACA	992
Qy	237	GCTTAGCGCCCTCAGCGGGTTACCTTCTCAGGCTTGCAAGATCTGGCCCTACACACTG	296

[illegible]

QY 1376 GTTGCTCTCTCTGTCATCAACAGACAGACAGCATTTTAATATTTAACTTATTTATTT 1435
| | | | |
Db 2133 GTTGCTCTCTCTGTCATCAACAGACAGACAGCATTTTAATATTTAACTTATTTATTT 2192
| | | | |
QY 1436 AACAAAGTAGAAGGAAATCCATTGCTAGCTTTTCTGTGTGTGTCTTAATATTTGGGTAG 1495
| | | | |
Db 2193 AACAAAGTAGAAGGAAATCCATTGCTAGCTTTTCTGTGTGTGTCTTAATATTTGGGTAG 2252
| | | | |
QY 1496 GGTGGGGGATCCCAACATCAGGTCCCTGAGATAGCTGTGATTTGGGTGATCATGTC 1555
| | | | |
Db 2253 GGTGGGGGATCCCAACATCAGGTCCCTGAGATAGCTGTGATTTGGGTGATCATGTC 2312
| | | | |
QY 1556 CAGAACTCTTCTCTCCCTGGGGTCTGGCCCAAAAGCTTAACCCAGAGACTTTGAAAT 1615
| | | | |
Db 2313 CAGAACTCTTCTCTCCCTGGGGTCTGGCCCAAAAGCTTAACCCAGAGACTTTGAAAT 2372
| | | | |
QY 1616 TCTACTCATCCCAATATATTCMAATGCTGTTCACCAAGGTAGGGGTGTGAAGAA 1675
| | | | |
Db 2373 TCTACTCATCCCAATATATTCMAATGCTGTTCACCAAGGTAGGGGTGTGAAGAA 2432
| | | | |
QY 1676 GGTAGAGGGTGGGCTTCAAGTCTCAACGGCTTCCCTAACCAACCCCTCTTCTTGGCC 1735
| | | | |
Db 2433 GGTAGAGGGTGGGCTTCAAGTCTCAACGGCTTCCCTAACCAACCCCTCTTCTTGGCC 2492
| | | | |
QY 1736 AGCTGGTTCCTCCCACTTCCCTCACTCCCTCTACTCTCTAGAGACTGGGGCTGATGAAGG 1795
| | | | |
Db 2493 AGCTGGTTCCTCCCACTTCCCTCACTCCCTCTACTCTCTAGAGACTGGGGCTGATGAAGG 2552
| | | | |
QY 1796 ACTGCCCAAAATTTCCCTTACCCCAACCTTCCCTTACCCCAACCTTCCCAACCTT 1855
| | | | |
Db 2553 ACTGCCCAAAATTTCCCTTACCCCAACCTTCCCTTACCCCAACCTTCCCAACCTT 2612
| | | | |
QY 1856 CACAACCTCTTGGAGCTCTGACAGACCAAGAGCAAAAGTGGCTTTCCCAAGCTT 1915
| | | | |
Db 2613 CACAACCTCTTGGAGCTCTGACAGACCAAGAGCAAAAGTGGCTTTCCCAAGCTT 2672
| | | | |
QY 1916 TGTTCATCTCAGCCCAAGATATCTGTGCTTGGGGAATCTCACAGAAATCTCAGGA 1975
| | | | |
Db 2673 TGTTCATCTCAGCCCAAGATATCTGTGCTTGGGGAATCTCACAGAAATCTCAGGA 2732
| | | | |
QY 1976 GCAACCCCTGCTGACTTAAAGGAGGTCTTATCTCTCAGGGGGGTTTAAAGTCCGTTTG 2035
| | | | |
Db 2733 GCAACCCCTGCTGACTTAAAGGAGGTCTTATCTCTCAGGGGGGTTTAAAGTCCGTTTG 2792
| | | | |
QY 2036 CATATATGCTGCTTATTTTATTTTAAAGGGGTGAATTTTATCTAGTAGTAGCAATCA 2095
| | | | |
Db 2793 CATATATGCTGCTTATTTTATTTTAAAGGGGTGAATTTTATCTAGTAGTAGCAATCA 2852
| | | | |
QY 2096 GAGTATATGTTTATGTTAGTGAACAATTTAAAGGCTTCTTATATGTTTAA 2143
| | | | |
Db 2853 GAGTATATGTTTATGTTAGTGAACAATTTAAAGGCTTCTTATATGTTTAA 2900
| | | | |
RESULT 8
AX200994 2904 bp DNA linear PAT 29-AUG-2001
LOCUS AX200994 Sequence 624 from Patent WO0151633.
DEFINITION AX200994
ACCESSION AX200994.1 GI:15390821
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS
1 Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
Reed, S.G., Kalos, M.D., Fanger, G.R., Day, C.H., Rether, M.W.,
Stolk, J.A., Skelky, Y.A., Wang, A. and Mesinger, M.J.
TITLE
Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL
Patent: WO 0151633-A 624 19-JUL-2001;
CORIXA CORPORATION (US)

FEATURES
source Location/Qualifiers
1..2904
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 89.4%; Score 1916; DB 6; Length 2904;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2086; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 57 GGCCTTCGATGGGAGACCTGGGCTGTTCCTGCACTGAGCCATCTCCCTGCTTCTCT 116
| | | | |
Db 813 GGCCTTCGATGGGAGACCTGGGCTGTTCCTGCACTGAGCCATCTCCCTGCTTCTCT 872
| | | | |
QY 117 CTGTCTATGAGACCGGCTGGTGCAGATTCGGCACTCGAGAGCTATTTGGCCAGTGG 176
| | | | |
Db 873 CTGTCTATGAGACCGGCTGGTGCAGATTCGGCACTCGAGAGCTATTTGGCCAGTGG 932
| | | | |
QY 177 GCAGCTTTCCTGTGGCTGGCCGCTGCACATGCTGTCCACAGTGTGGCCGTGTGACA 236
| | | | |
Db 933 GCAGCTTTCCTGTGGCTGGCCGCTGCACATGCTGTCCACAGTGTGGCCGTGTGACA 992
| | | | |
QY 237 GCTTACGCGGCTTACCGGGGTTCACTTTCAGGCTTGCAGATTCCTGCTTACACATG 296
| | | | |
Db 993 GCTTACGCGGCTTACCGGGGTTCACTTTCAGGCTTGCAGATTCCTGCTTACACATG 1052
| | | | |
QY 297 GCTTCCCTTACCAACCGGAGAGAGAGGTGTTCCTGCCCAATATCCGAGGAGACACTGA 356
| | | | |
Db 1053 GCTTCCCTTACCAACCGGAGAGAGAGGTGTTCCTGCCCAATATCCGAGGAGACACTGA 1112
| | | | |
QY 357 GGTGTCTACAGTGAAGACAGCTGATGACAGCTTCTGTCCAGAGCCTTAAGCTTGAAGT 416
| | | | |
Db 1113 GGTGTCTACAGTGAAGACAGCTGATGACAGCTTCTGTCCAGAGCCTTAAGCTTGAAGT 476
| | | | |
QY 417 CCTTCCCTTAAATGACAGTGGGTGTGAGAGAGAGGCTGCTCCACCTTCCACCCGCG 476
| | | | |
Db 1113 CCTTCCCTTAAATGACAGTGGGTGTGAGAGAGAGGCTGCTCCACCTTCCACCCGCG 1232
| | | | |
QY 477 CTGTGCGGGGCTTCTGCTGTGATGTCTCCGTACGTGTGTGTGTGTGAGCCCAAGAG 536
| | | | |
Db 1233 CTGTGCGGGGCTTCTGCTGTGATGTCTCCGTACGTGTGTGTGTGTGAGCCCAAGAG 1292
| | | | |
QY 537 GCAAGGGGTGTCCGGGCGGGGCGGATCTGCTGTGACCTTCGCACTCTGATAGTGGCTTC 596
| | | | |
Db 1293 GCAAGGGGTGTCCGGGCGGGGCGGATCTGCTGTGACCTTCGCACTCTGATAGTGGCTTC 1352
| | | | |
QY 597 CTGTGCTCCAGTGGCCCATCCCTGTTTATGGGCTCAATTGTCAGCTCAGCCAGTCT 656
| | | | |
Db 1353 CTGTGCTCCAGTGGCCCATCCCTGTTTATGGGCTCAATTGTCAGCTCAGCCAGTCT 1412
| | | | |
QY 657 GTCACTGCTTATATGATGTCTGCGCGAGGCTGGGCTTGTGTGCAATTTACTTGTCA 716
| | | | |
Db 1413 GTCACTGCTTATATGATGTCTGCGCGAGGCTGGGCTTGTGTGCAATTTACTTGTCA 1472
| | | | |
QY 717 CAGGTATGATTTGACAGAGGACTTGGGCAATATCAAGGTATGAGAACTTCCAGACA 776
| | | | |
Db 1473 CAGGTATGATTTGACAGAGGACTTGGGCAATATCAAGGTATGAGAACTTCCAGACA 1532
| | | | |
QY 777 TTGGGGTGAAGGGCTGCTCACTGAGTTCACAGTTCCTCCGCTCTGTAAAGCCCATGGG 836
| | | | |
Db 1533 TTGGGGTGAAGGGCTGCTCACTGAGTTCACAGTTCCTCCGCTCTGTAAAGCCCATGGG 1592
| | | | |
QY 837 CTGCGGGGCTGGCGCGCAATTTCTGTGTGCTCCCAAGTATGTGGCTCTGTGCTGCACC 896
| | | | |
Db 1593 CTGCGGGGCTGGCGCGCAATTTCTGTGTGCTCCCAAGTATGTGGCTCTGTGCTGCACC 1652
| | | | |
QY 897 CTGTGCTGTAAGGTGTGATGCTGACAGTGTGGGGGCTGGGGGCTCTCTCTCTCC 956
| | | | |
Db 1653 CTGTGCTGTAAGGTGTGATGCTGACAGTGTGGGGGCTGGGGGCTCTCTCTCTCC 1712
| | | | |
QY 957 CCACTCTTGAAGGCTGCTGACTGAGAGGCTTCCAAAGGGGTTCACTGTGACTTATAC 1016
| | | | |


```

Oy 597 CTGCTGTCACAGGTGGGCCCCCATCCCTGTTTATGAGGCTTCATTGTCAGCTCAGCCAGTCT 656
Db 1353 CTGCTGTCACAGGTGGGCCCCCATCCCTGTTTATGAGGCTTCATTGTCAGCTCAGCCAGTCT 1412
Oy 657 GTCACTGCTTATATGAGTGTCTGCGCAGAGGCTGGGCTCTGTCGACATTTATCTTTGCTACA 716
Db 1413 GTCACTGCTTATATGAGTGTCTGCGCAGAGGCTGGGCTCTGTCGACATTTATCTTTGCTACA 1472
Oy 717 CAGGTAGTATTTGACAAAGAGGACTTGGCCAAATATCTCAGGTAGAAATCTTCAGACACA 776
Db 1473 CAGGTAGTATTTGACAAAGAGGACTTGGCCAAATATCTCAGGTAGAAATCTTCAGACACA 1532
Oy 777 TTGGGAGTGAAGGAGGCTGCTCAGTGGGTCAGAGTCCCGGCTCTGTTAGCCCAATGAGG 836
Db 1533 TTGGGAGTGAAGGAGGCTGCTCAGTGGGTCAGAGTCCCGGCTCTGTTAGCCCAATGAGG 1592
Oy 837 CTGCGGGAGTGGCGCCAGATTTCTGTTGTCGCCAAAGTAAATGAGGCTCTGTCGTCACAC 896
Db 1593 CTGCGGGAGTGGCGCCAGATTTCTGTTGTCGCCAAAGTAAATGAGGCTCTGTCGTCACAC 1652
Oy 897 CTGTCGTCGAGAGTGGGTCGTCAGACAGCTGGGAGGCTGGGAGGCTCTCTCTCTCTCC 956
Db 1653 CTGTCGTCGAGAGTGGGTCGTCAGACAGCTGGGAGGCTGGGAGGCTCTCTCTCTCTCC 1712
Oy 957 CCACTCTCTAAGGCTGCTGCTGACCTGAGAGGCTTCCAAAGGAGGTTTCAAGTCTGACTTATAC 1016
Db 1713 CCACTCTCTAAGGCTGCTGCTGACCTGAGAGGCTTCCAAAGGAGGTTTCAAGTCTGACTTATAC 1772
Oy 1017 AGGAGGSCCAAGAGGAGGCTCCATGACCTGGAATGC - GGAATCTGTCAGGTGATTAACCCAG 1075
Db 1773 AGGAGGSCCAAGAGGAGGCTCCATGACCTGGAATGCAGGAGACTCGCAGGTGATTAACCCAG 1832
Oy 1076 GCTCAGGAGTTAAGAGTACGCTCTGATTGAGACACACCTAGAGAGGAGGTTTTGGGAGC 1135
Db 1833 GCTCAGGAGTTAAGAGTACGCTCTGATTGAGACACACCTAGAGAGGAGTTTTGGGAGC 1892
Oy 1136 TGAATTAACCTGACCTGCTGTTCCCATCTCTAAGCCCCCTTAACCTGACGCTTGTTA 1195
Db 1893 TGAATTAACCTGACCTGCTGTTCCCATCTCTAAGCCCCCTTAACCTGACGCTTGTTA 1952
Oy 1196 ATGTAGCTCTTGCATGGAGGTTTCTAGATGAACAACCTCTCATGAGGATTTGAACATAT 1255
Db 1953 ATGTAGCTCTTGCATGGAGGTTTCTAGATGAACAACCTCTCATGAGGATTTGAACATAT 2012
Oy 1256 GAAAGTATTTTGAAGGAGGAGTCTGAGGAGCAACACAAAGAACAGGCTCCCTCAG 1315
Db 2013 GAAAGTATTTTGAAGGAGGAGTCTGAGGAGCAACACAAAGAACAGGCTCCCTCAG 2072
Oy 1316 CCCACAGCACTGCTTTTGTGCTGATCCACCCCCCTTCTTACTTTATCAGATGAGGCT 1375
Db 2073 CCCACAGCACTGCTTTTGTGCTGATCCACCCCCCTTCTTACTTTATCAGATGAGGCT 2132
Oy 1376 GTTGTGCTTCTGTTGTCATCAAGAGACAGAGGCTTAAATATTTAACTATTATTT 1435
Db 2133 GTTGTGCTTCTGTTGTCATCAAGAGACAGAGGCTTAAATATTTAACTATTATTT 2192
Oy 1436 AACCAAGTGAAGGAGATCATTTGCTAGCTTTTCTGTGTGTCTAATAATTTGGGTAG 1495
Db 2193 AACCAAGTGAAGGAGATCATTTGCTAGCTTTTCTGTGTGTCTAATAATTTGGGTAG 2252
Oy 1496 GGTGGGGAGTCCCAACATCAGGTCCTCTGATAGCTGTCGTCGATTTGGGCTGATTCG 1555
Db 2253 GGTGGGGAGTCCCAACATCAGGTCCTCTGATAGCTGTCGTCGATTTGGGCTGATTCG 2312
Oy 1556 CAGAACTTTTCTCTCTGGGCTCTGGCCCCCAAAATGCTTAAACCCAGACCTTGGAAAT 1615
Db 2313 CAGAACTTTTCTCTCTGGGCTCTGGCCCCCAAAATGCTTAAACCCAGACCTTGGAAAT 2372
Oy 1616 TCTACTCATCCCAATGATTAATTTCCAATGCTGTTTACCCAAAGTTAGGTTGAGAGAA 1675
Db 2373 TCTACTCATCCCAATGATTAATTTCCAATGCTGTTTACCCAAAGTTAGGTTGAGAGAA 2432
Oy 1676 GGTAGAGGAGTGGGCTTCAAGTCTCAAGGCTTCCCTTAACAACCCCTTCTCTGGCCC 1735

```

```

Db 2433 GGTAGAGGAGTGGGCTTCAAGTCTCAAGGCTTCCCTTAACAACCCCTTCTCTGGCCC 2492
Oy 1736 AGCTGGTTCCTCCCACTTCCACTCCCTCTTACTCTCTGAGACTGGGCTGATGAAGC 1795
Db 2493 AGCTGGTTCCTCCCACTTCCACTCCCTCTTACTCTCTGAGACTGGGCTGATGAAGC 2552
Oy 1796 ACTGGCCAAATTTTCCCTCAACCCCACTTCCCTCAACCCCACTTCCCTCAACAGTC 1855
Db 2553 ACTGGCCAAATTTTCCCTCAACCCCACTTCCCTCAACCCCACTTCCCTCAACAGTC 2612
Oy 1856 CACAACCTGTTTGAAGTCTGACAGACCAAGACCAAAAGTGGGTTTCCCAAGCTT 1915
Db 2613 CACAACCTGTTTGAAGTCTGACAGACCAAGACCAAAAGTGGGTTTCCCAAGCTT 2672
Oy 1916 TGTCCATCTCAGCCCCCAGAGTATATCTGCTTGGGAAATCTCACAAGAACTCAGGA 1975
Db 2673 TGTCCATCTCAGCCCCCAGAGTATATCTGCTTGGGAAATCTCACAAGAACTCAGGA 2732
Oy 1976 GCACCCCTGCTGAGTGAAGGAGGCTTATCTCTCAGGAGGAGTAAATGAGGCTTGG 2035
Db 2733 GCACCCCTGCTGAGTGAAGGAGGCTTATCTCTCAGGAGGAGTAAATGAGGCTTGG 2792
Oy 2036 CAATTAATGCTCTTATTTTATGCGGAGTGAATTTTAACTGTAAGTGAACAATCA 2095
Db 2793 CAATTAATGCTCTTATTTTATGCGGAGTGAATTTTAACTGTAAGTGAACAATCA 2852
Oy 2096 GAGTAAATGTTTATGAGTGAACAATTAAGGCTTCTTATATGTTA 2143
Db 2853 GAGTAAATGTTTATGAGTGAACAATTAAGGCTTCTTATATGTTA 2900

```

```

RESULT 10
AA327336
LOCUS AA327336 3320 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 1 from Patent WO0181577.
ACCESSION AA327336
VERSION AA327336.1 GI:18097882
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Lau, T., Lin, R.J., Parkes, D., Parry, G., Schneider, D.W.,
Seidbrecher, R., van Heult, P.T. and Wu, J.
Dna encoding the prost 03 polypeptide
Patent: WO 0181577-A 1 01-NOV-2001;
SCHERING AKTIEGENSCHAFT (DE)
FEATURES
source
1..3320
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
282..1943
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD20424.1"
/db_xref="GI:18097883"
/translation="MVQRLVSRLLRHRKAQLLVNLIFGLVCLAAGITVYPPLL
EYVEREKFTMTVIGIPVLGIVCPILGASDHMRGRGRRPFTALISGLISLFL
IPRAGLILGCPDRPLELALLIIGVGLDSCGQCTPLRLLISDLPRPDHROA
YGVVAMVSLIGGLCYLLPAIDWDPSALAPYIGTBECLFGLITLFLTCVATLLVA
EERAAIPTPAGLAPSLSPSCCECRARLARINIGALLPRHQICSMPTURLLV
AEICSMALMTTLFTYTFVSGGLVQVPRAPGTEBARHVDGVRMOSLGLFLOCAI
SLVFLVMDRLVQRTAVLYASVAAFPVAGATCLSHSVAVVYASALNGFTSAL
QILPYTLASLYHREKQVLEPKRQDTGASDSLSMTSFLRQPKGAPLNGVAGG
SGLPPLPCASADSVSRVYVVEPTEARVPERGI CLDIALIDSAPFLISQVAPSL
FMGSLVQSLQSTAYTAVMSAAGLVAIIFATQVVRKSDKLKYS"

```

ORIGIN

```

Query Match 88.7%; Score 1900; DB 6; Length 3320;
Best Local Similarity 100.0%; Pred. No. 0;

```

Matches 2020; Conservative 0; Mismatches 0; Indels 1; Gaps 1;				
QY	1	ACGAGGCGCTGCCAGAGCTGAGCCGGGACCGAGGCCCGGAGACATATGATGAAGCG	60	
DB	1183	ACCAGGCGCTGGCCAGAGCTGAGCCGGGACCGAGGCCCGGAGACACTATGATGAAGCG	1242	
QY	61	TTCCGATGGGACGCTGGGGCTGTTCTGCAAGTGGGCACTCCCGGTCTTCTCTCG	120	
DB	1243	TTCCGATGGGACGCTGGGGCTGTTCTGCAAGTGGGCACTCCCGGTCTTCTCTCG	1302	
QY	121	TCATGAGCCGGCTGTGTGACAGCATTCGGCACTGAGCAGTCTATTTGGCAGTGGCAG	180	
DB	1303	TCATGAGCCGGCTGTGTGACAGCATTCGGCACTGAGCAGTCTATTTGGCAGTGGCAG	1362	
QY	181	CTTTTCCCTGTGCTGCGGCTGCCACATGCTCTGTCCCAAGTGTGCTGTGTGACAGCTT	240	
DB	1363	CTTTTCCCTGTGCTGCGGCTGCCACATGCTCTGTCCCAAGTGTGCTGTGTGACAGCTT	1422	
QY	241	CAGCGGCGCTCACCGGGTTCACCTTGTCAAGCCCTGAGATCCCTGCTTACACATGGGCT	300	
DB	1423	CAGCGGCGCTCACCGGGTTCACCTTGTCAAGCCCTGAGATCCCTGCTTACACATGGGCT	1482	
QY	301	CCCTTACCAACCGGAGAGAGAGTGTCTGCGCCAAATACGAGGGGACATGAGAGTG	360	
DB	1483	CCCTTACCAACCGGAGAGAGAGTGTCTGCGCCAAATACGAGGGGACATGAGAGTG	1542	
QY	361	CTAGCAGTAGAGACAGCTGTATGACAGCTTCTCTGCAAGCCCTTAAAGCTGTGCTCT	420	
DB	1543	CTAGCAGTAGAGACAGCTGTATGACAGCTTCTCTGCAAGCCCTTAAAGCTGTGCTCT	1602	
QY	421	TCCCTAATGGACACGTTGGGTGCTGAGGAGAGTGGCTGTCCCACTTCAACCGGCTGT	480	
DB	1603	TCCCTAATGGACACGTTGGGTGCTGAGGAGAGTGGCTGTCCCACTTCAACCGGCTGT	1662	
QY	481	GCGGGGCTCTGCTGTGTGTCTCCGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	540	
DB	1663	GCGGGGCTCTGCTGTGTGTCTCCGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1722	
QY	541	GCGGTGTTCCGGGACCGGGGCTGTGCTGAGACCTGTGCACTCTGTATGTGCTTCTG	600	
DB	1723	GCGGTGTTCCGGGACCGGGGCTGTGCTGAGACCTGTGCACTCTGTATGTGCTTCTG	1782	
QY	601	TGTCCAGGTGGCCCATCTCTGTTTATGAGGCTTCAATGTCCAGCTCAACAGCTGTGTA	660	
DB	1783	TGTCCAGGTGGCCCATCTCTGTTTATGAGGCTTCAATGTCCAGCTCAACAGCTGTGTA	1842	
QY	661	CTGCTATATGTGTGTGTGCGAGGCTGGGTCTGTGCGCAATTTACTTTGCTACACAG	720	
DB	1843	CTGCTATATGTGTGTGTGCGAGGCTGGGTCTGTGCGCAATTTACTTTGCTACACAG	1902	
QY	721	TAGTATTGACAAAGCGACTTGGCCAAATACTCAGCTGTAGAAAATTTCCAGACATTGG	780	
DB	1903	TAGTATTGACAAAGCGACTTGGCCAAATACTCAGCTGTAGAAAATTTCCAGACATTGG	1962	
QY	781	GGTGAAGGGGCTGCTCACTGGGTCCAGCTCCCGCTCTGTGAGCCCAAGGGGCTGC	840	
DB	1963	GGTGAAGGGGCTGCTCACTGGGTCCAGCTCCCGCTCTGTGAGCCCAAGGGGCTGC	2022	
QY	841	CGGGCTGCGCGCAGTTTCTGTTGTGCGAAAGTATGTGGCTCTGTGCGACCCCTGT	900	
DB	2023	CGGGCTGCGCGCAGTTTCTGTTGTGCGCGAAAGTATGTGGCTCTGTGCGACCCCTGT	2082	
QY	901	GCTGCTGAGGTGCTGATGCTGACAGTGGGGGCTGGGGGCTCTCTCTCTCTCCCG	960	
DB	2083	GCTGCTGAGGTGCTGATGCTGACAGTGGGGGCTGGGGGCTCTCTCTCTCTCCCG	2142	
QY	961	TCTCTAAGGCTGCTGACAGTGGGCTTCCAAAGGGGCTTCACTGTGACCTTATACAGG	1020	
DB	2143	TCTCTAAGGCTGCTGACAGTGGGCTTCCAAAGGGGCTTCACTGTGACCTTATACAGG	2202	
QY	1021	AGGCCAGAAAGGCTCCATGCTCACTGTGATGC-GGAACTGTGAGGTGATTAACCAAGCTC	1079	
DB	2203	AGGCCAGAAAGGCTCCATGCTCACTGTGATGC-GGAACTGTGAGGTGATTAACCAAGCTC	2262	

QY	1080	AGGTTTAAAGCTTACCTTCTATGTTGACACACCTTACAGAAAGGTTTTTGGAGCTGA	1139	
DB	2263	AGGTTTAAAGCTTACCTTCTATGTTGACACACCTTACAGAAAGGTTTTTGGAGCTGA	2322	
QY	1140	TAAACTCACTACCTGTTTTTCCATCTCTTAAGCCCTTAAACCTGAGCTCGTTAAATG	1199	
DB	2323	TAAACTCACTACCTGTTTTTCCATCTCTTAAGCCCTTAAACCTGAGCTCGTTAAATG	2382	
QY	1200	AGCTTTGATGGAGTTTCTAGATGAACACTCTCCATGGAGTTTGAACATATGAA	1259	
DB	2383	AGCTTTGATGGAGTTTCTAGATGAACACTCTCCATGGAGTTTGAACATATGAA	2442	
QY	1260	GTTATTTTGAAGGGAGAGTCTGTAGGGGCAACACAGAAACAGTCTCCCTCAGCCCA	1319	
DB	2443	GTTATTTTGAAGGGAGAGTCTGTAGGGGCAACACAGAAACAGTCTCCCTCAGCCCA	2502	
QY	1320	CAGCATGTCTTTTGTGATGACACCCCTCTTACCTTTATCAAGATGGGCTGTG	1379	
DB	2503	CAGCATGTCTTTTGTGATGACACCCCTCTTACCTTTATCAAGATGGGCTGTG	2562	
QY	1380	GTCCTTGTGTGTCATACAGAGACACAGGCAATTTAAATTTAACTTATTTTAAACA	1439	
DB	2563	GTCCTTGTGTGTCATACAGAGACACAGGCAATTTAAATTTAACTTATTTTAAACA	2622	
QY	1440	AAGTGAAGGGAATCAATGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1499	
DB	2623	AAGTGAAGGGAATCAATGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2682	
QY	1500	GGGGAATCCCAACATTCAGGTCCCGGAGATGCTGTGATGCTGATGGCTGATCCACA	1559	
DB	2683	GGGGAATCCCAACATTCAGGTCCCGGAGATGCTGTGATGCTGATGGCTGATCCACA	2742	
QY	1560	ATCTTCTTCTCTGAGGCTGTGAGCCGCCCAAAATGCTTAAACCAAGACCTTGAATTTCTA	1619	
DB	2743	ATCTTCTTCTCTGAGGCTGTGAGCCGCCCAAAATGCTTAAACCAAGACCTTGAATTTCTA	2802	
QY	1620	CTCATCCCAATGATTAATTCCAATGCTGTTAACCAAGTTAGGTTGTGAAGAGTGA	1679	
DB	2803	CTCATCCCAATGATTAATTCCAATGCTGTTAACCAAGTTAGGTTGTGAAGAGTGA	2862	
QY	1680	GAGGGTGGGGCTTCAAGGTCTCAAGGCTTCCCTAACACCCCTCTTCTTGGGCCAGGC	1739	
DB	2863	GAGGGTGGGGCTTCAAGGTCTCAAGGCTTCCCTAACACCCCTCTTCTTGGGCCAGGC	2922	
QY	1740	TGTTTCCCCCACTTCACTCCCTCTACTCTCTTGAAGACTGGCTGATGAAGCACTG	1799	
DB	2923	TGTTTCCCCCACTTCACTCCCTCTACTCTCTTGAAGACTGGCTGATGAAGCACTG	2982	
QY	1800	CCCAAAATTTCCCTTACCCCACTTTTCCCTTACCCCACTTTTCCCAACAGCTTCACA	1859	
DB	2983	CCCAAAATTTCCCTTACCCCACTTTTCCCTTACCCCACTTTTCCCAACAGCTTCACA	3042	
QY	1860	ACCCGTTTGAAGTACTGACAGAGACAGAGACAAAGTGGGTTTCCCAAGCCTTGTGC	1919	
DB	3043	ACCCGTTTGAAGTACTGACAGAGACAGAGACAAAGTGGGTTTCCCAAGCCTTGTGC	3102	
QY	1920	CATCTCAGCCCCAGAGTATATCTGTGCTTGGGAAATCTCACACAGAACTCAGAGAC	1979	
DB	3103	CATCTCAGCCCCAGAGTATATCTGTGCTTGGGAAATCTCACACAGAACTCAGAGAC	3162	
QY	1980	CCCCTGCTGAGCTTAAAGGAGTCTTATCTCTCAGGGGGGG	2020	
DB	3163	CCCCTGCTGAGCTTAAAGGAGTCTTATCTCTCAGGGGGGG	3203	

RESULT 11
AR278711 4034 bp DNA linear PAT 10-APR-2003
LOCUS AR278711
DEFINITION Sequence 704 from patent US 6512094.
ACCESSION AR278711
VERSION AR278711.1 GI:29712957
KEYWORDS

Db 3802 TTGTCAATTCAGCCCCCGAGATATATCTGTCTTGGGAAATCTCACAGAAATCTCAG 3861
Qy 1975 AGCACCCCTGCTGCTAGCTAAGAGAGTCTTATCTCTCAGGGGGGTTTAACTGCCGTT 2034
Db 3862 AGCACCCCTGCTGCTAGCTAAGAGAGTCTTATCTCTCAGGGGGGTTTAACTGCCGTT 3921
Qy 2035 GCAATTAATGCTGCTTATTTTATTTTATAGCGGGGTAATTTTATTAATCTAAGTGAAGCAATC 2094
Db 3922 GCAATTAATGCTGCTTATTTTATTTTATAGCGGGGTAATTTTATTAATCTAAGTGAAGCAATC 3981
Qy 2095 AGAGTATAATGTTTATAGTGAACAAATTAAGGCTTTCTTATATGTTTA 2143
Db 3982 AGAGTATAATGTTTATAGTGAACAAATTAAGGCTTTCTTATATGTTTA 4030
RESULT 12
AR400443 4034 bp DNA linear PAT 18-DEC-2003
LOCUS AR400443
DEFINITION Sequence 704 from patent US 6620922.
ACCESSION AR400443
VERSION AR400443.1 GI:40143820
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4034)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kales,M.D., Fanger,G.R., Reiter,M.W., Stolk,J.A., Day,C.H.,
Vedlik,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITILE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6620922-A 704 16-SEP-2003;
FEATURES
source Location/Qualifiers
1..4034
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 83.8%; Score 1796; DB 6; Length 4034;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2086; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
Qy 56 AGCGCTTGGATGGGAGCGCTTGGGCTGTTCTGCTGAGTGGCCATCTCCCTGCTTCTC 115
Db 1943 AGCGCTTGGATGGGAGCGCTTGGGCTGTTCTGCTGAGTGGCCATCTCCCTGCTTCTC 2002
Qy 116 TCTGTGATGAGACCGGCTGCTGATGAGATTCGGCACTCGAGAGTCTATTTGGCAGTGT 175
Db 2003 TCTGTGATGAGACCGGCTGCTGATGAGATTCGGCACTCGAGAGTCTATTTGGCAGTGT 2062
Qy 176 GGCAGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 235
Db 2063 GGCAGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2122
Qy 236 AGCTTACGCGCCCTCAACCGGGTCACTTCTCAAGCTTGCAGATCTGCTCCCTACACT 295
Db 2123 AGCTTACGCGCCCTCAACCGGGTCACTTCTCAAGCTTGCAGATCTGCTCCCTACACT 2182
Qy 296 GGCCTCCCTCTACACCGGGAGAGAGGTTTCCGSCCAATACCGAGGGGAGCACTGG 355
Db 2183 GGCCTCCCTCTACACCGGGAGAGAGGTTTCCGSCCAATACCGAGGGGAGCACTGG 2242
Qy 356 AGGTGTACAGTGAAGAGAGCTGATGACAGCTTCTGCAAGGCTTAAAGCTTGAAGC 415
Db 2243 AGGTGTACAGTGAAGAGAGCTGATGACAGCTTCTGCAAGGCTTAAAGCTTGAAGC 2302
Qy 416 TCCCTTCCCTTAATGACAGTGGGTCTGAGAGCAAGTGGCTGCTCCACCTTCACCGC 475
Db 2303 TCCCTTCCCTTAATGACAGTGGGTCTGAGAGCAAGTGGCTGCTCCACCTTCACCGC 2362
Qy 476 GCTCTGCGGGGCTGCTGCTGATGTCTCCGTAAGTGTGTGGTGGTGAAGCCACGA 535

Db 2363 GCTCTGCGGGGCTGCTGCTGATGTCTCCGTAAGTGTGTGGTGGTGAAGCCACGA 2422
Qy 536 GGCAGAGGTGATTCGCGGCGGGGAGCATCTGCTGAGCCTCGGCATCTTGATAGTGCCT 595
Db 2423 GGCAGAGGTGATTCGCGGCGGGGAGCATCTGCTGAGCCTCGGCATCTTGATAGTGCCT 2482
Qy 596 CCTGCTGCTCCAGAGTGGCCCATCCCTGTTTATGGGCTTCATTTGTCAGCTCAGCCAGTC 655
Db 2483 CCTGCTGCTCCAGAGTGGCCCATCCCTGTTTATGGGCTTCATTTGTCAGCTCAGCCAGTC 2542
Qy 656 TGTCACTGCTTATAGTGTCTGAGCCAGAGCCTGGGCTGCTGTCGCACTTACTTGTCTAC 715
Db 2543 TGTCACTGCTTATAGTGTCTGAGCCAGAGCCTGGGCTGCTGTCGCACTTACTTGTCTAC 2602
Qy 716 ACAGGTAGTATTGACAAAGAGCACTGCGCAATATCTCAGGTAGAAATCTTCAGCAGC 775
Db 2603 ACAGGTAGTATTGACAAAGAGCACTGCGCAATATCTCAGGTAGAAATCTTCAGCAGC 2662
Qy 776 ATTTGGGGTGAAGGGCTGCTGCTCACTGGGTCCAGCTCCCGCTCCTGTTAAGCCCATGGG 835
Db 2663 ATTTGGGGTGAAGGGCTGCTGCTCACTGGGTCCAGCTCCCGCTCCTGTTAAGCCCATGGG 2722
Qy 836 GCTGCGGGGCTGCGCCAGCTTCTGTTGCTGCGCAAGATATGTGAGCTCTGCTGCGCAG 895
Db 2723 GCTGCGGGGCTGCGCCAGCTTCTGTTGCTGCGCAAGATATGTGAGCTCTGCTGCGCAG 2782
Qy 896 CCTGTGCTGCTGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 955
Db 2783 CCTGTGCTGCTGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2842
Qy 956 CCCAGTCTCTAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1015
Db 2843 CCCAGTCTCTAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2902
Qy 1016 CAGGAGGCGCAAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1074
Db 2903 CAGGAGGCGCAAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2962
Qy 1075 GGCCTCAGGTTTAAACAGCTAGCCTCTCTAGTTGAGACACCTTGAAGAGGTTTTGGAG 1134
Db 2963 GGCCTCAGGTTTAAACAGCTAGCCTCTCTAGTTGAGACACCTTGAAGAGGTTTTGGAG 3022
Qy 1135 CTGAATTAATCTGATCACTGCTTCCATCTCTAAGCCCTTAACTGACACTTCTGTT 1194
Db 3023 CTGAATTAATCTGATCACTGCTTCCATCTCTAAGCCCTTAACTGACACTTCTGTT 3082
Qy 1195 AATGTAGCTCTTGCATGGAGTTTCTAGAGTAAACACTCTCCATGGGATTTGAACATA 1254
Db 3083 AATGTAGCTCTTGCATGGAGTTTCTAGAGTAAACACTCTCCATGGGATTTGAACATA 3142
Qy 1255 TGAATGATTTTGTAGGGAGAGTCTGAGGGGAGCAACACAGAACAGAGTCCCTCA 1314
Db 3143 TGAATGATTTTGTAGGGAGAGTCTGAGGGGAGCAACACAGAACAGAGTCCCTCA 3202
Qy 1315 GCCCAGACAGTCTTCTTTTGTGATTCACCCCTCTTAACTTTTATCAGATGTGGC 1374
Db 3203 GCCCAGACAGTCTTCTTTTGTGATTCACCCCTCTTAACTTTTATCAGATGTGGC 3261
Qy 1375 TGTGTGCTCTGTTGTCATCAGAGAGCAAGGCACTTAAATTAATTAATTAATTTAT 1434
Db 3262 TGTGTGCTCTGTTGTCATCAGAGAGCAAGGCACTTAAATTAATTAATTAATTTAT 3321
Qy 1435 TAACAAGTAGAAGGAATTCATTCCTAGCTTTCTGTGTGTGTCTTAATATTTGGGTA 1494
Db 3322 TAACAAGTAGAAGGAATTCATTCCTAGCTTTCTGTGTGTGTCTTAATATTTGGGTA 3381
Qy 1495 GGGTGGGGATCCCAACAAATAGGTCCCTGAGATAGTGTCTATTTGGGCTGATCATTTG 1554
Db 3382 GGGTGGGGATCCCAACAAATAGGTCCCTGAGATAGTGTGTCTATTTGGGCTGATCATTTG 3441
Qy 1555 CCAGATCTTCTCTCTGCGGCTGCGCCCCCAAAATGCTTAACCCAGAGACTTGGAAA 1614

Db 3442 CCAGATCTCTCTCTCTGAGGCTGAGCCCCCAAAAGCCTAACCGAGACTTGGAAA 3501
Qy 1615 TTCTACTATCCCAAAATGATTAATTCCTAAATGCTGTATCCAGGTAGGGTGTGAAGA 1674
Db 3502 TTCTACTATCCCAAAATGATTAATTCCTAAATGCTGTATCCAGGTAGGGTGTGAAGA 3561
Qy 1675 AGTAGAGGGTGGGGCTTCAGGTCTCAACGAGCTTCCCTAACCAACCCCTCTCTGGCC 1734
Db 3562 AGTAGAGGGTGGGGCTTCAGGTCTCAACGAGCTTCCCTAACCAACCCCTCTCTGGCC 3621
Qy 1735 CAGCTGGTTCCTCCCACTTCACTCCCTCTACTCTCTCTAGAGACTGGCTGATGAAG 1794
Db 3622 CAGCTGGTTCCTCCCACTTCACTCCCTCTACTCTCTAGAGACTGGCTGATGAAG 3681
Qy 1795 CAGTGGCCAAATTTCCCTCTACCTCCCACTTCCCTAACCCCACTTCCCAAGCT 1854
Db 3682 CAGTGGCCAAATTTCCCTCTACCTCCCACTTCCCTAACCCCACTTCCCAAGCT 3741
Qy 1855 CCACACCTCTGTTTGAAGCTACTGACAGACCCAGACCAAGTGCAGTTTCCCAAGCT 1914
Db 3742 CCACACCTCTGTTTGAAGCTACTGACAGACCCAGACCAAGTGCAGTTTCCCAAGCT 3801
Qy 1915 TTGTCCATCTCAGCCCCCAAGATATCTGTGCTGGAGATCTCACAGAAATCTCAG 1974
Db 3802 TTGTCCATCTCAGCCCCCAAGATATCTGTGCTGGAGATCTCACAGAAATCTCAG 3861
Qy 1975 AGCACCCCTGCTGAGCTAAGGAGGTCTTATCTCAGAGGGGGGTTTAAAGTCCGCTT 2034
Db 3862 AGCACCCCTGCTGAGCTAAGGAGGTCTTATCTCAGAGGGGGGTTTAAAGTCCGCTT 3921
Qy 2035 GCAATATGTCGCTTATTTTATTTTAAAGGGGTGAATTTTAACTGTAAAGTGAATC 2094
Db 3922 GCAATATGTCGCTTATTTTATTTTAAAGGGGTGAATTTTAACTGTAAAGTGAATC 3981
Qy 2095 AGAGTAAATGTTATGATGACAAATTTAAAGCTTCTTATATGTTTA 2143
Db 3982 AGAGTAAATGTTATGATGACAAATTTAAAGCTTCTTATATGTTTA 4030

RESULT 13
AR405710 4034 bp DNA 1linear PAT 18-DEC-2003
LOCUS Sequence 704 from patent US 6630305.
DEFINITION AR405710
ACCESSION AR405710
VERSION AR405710.1 GI:40154547
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4034)
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kaidor,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6630305-A 704 '07-OCT-2003;
FEATURES Location/Qualifiers
source 1..4034
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 83.8%; Score 1796; DB 6; Length 4034;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2086; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

Qy 56 AGGCGTTGGATGGGCAAGCTGGGGCTGTCTCTGAGGCGCATCTCCCTGCTTCTC 115
Db 1943 AGGCGTTGGATGGGCAAGCTGGGGCTGTCTCTGAGGCGCATCTCCCTGCTTCTC 2002
Qy 116 TCTGCTATGACCGGGCTGTGACCGATTCGGCACTGAGCAGCTTATTTGGCAGTGT 175

Db 2003 TCTGCTATGACCGGGCTGTGACCGATTCGGCACTGAGCAGCTTATTTGGCAGTGT 2062
Qy 176 GGCAGCTTTCCTGTGCTGCGGTCGACCAATGCTTCCCAAGTGTGGCGGTGTAC 235
Db 2063 GGCAGCTTTCCTGTGCTGCGGTCGACCAATGCTTCCCAAGTGTGGCGGTGTAC 2122
Qy 236 AGCTTACGCGGCTTCACCGGGTTCACCTTCTCAGCCCTGAGATCTGCTTACACACT 295
Db 2122 AGCTTACGCGGCTTCACCGGGTTCACCTTCTCAGCCCTGAGATCTGCTTACACACT 2182
Qy 296 GGCCTCCCTTACCAACCGGGAAGAGCAGTGTTCCTGCCCCAATTCGAGGGGACACTGG 355
Db 2183 GGCCTCCCTTACCAACCGGGAAGAGCAGTGTTCCTGCCCCAATTCGAGGGGACACTGG 2242
Qy 356 AGTGTGACAGTGAAGACAGCTGATGACCAAGCTTCTGACAGGCTTAAGCTTGAAGC 415
Db 2243 AGTGTGACAGTGAAGACAGCTGATGACCAAGCTTCTGACAGGCTTAAGCTTGAAGC 2302
Qy 416 TCCCTTCCCTAATGACACGTGGGTGCTGAGGACATGAGCTGCTCCACCTGCACCCGC 475
Db 2303 TCCCTTCCCTAATGACACGTGGGTGCTGAGGACATGAGCTGCTCCACCTGCACCCGC 2362
Qy 476 GCTCTGCGGGCTCTGCTGCTGATGATCTCCGTACGTGTGGTGGGTGAGCCACCGA 535
Db 2363 GCTCTGCGGGCTCTGCTGCTGATGATCTCCGTACGTGTGGTGGGTGAGCCACCGA 2422
Qy 536 GGCAGAGGTGTTCCGGGCGGGGCATCTGCTGAGACCTGCACCTCGATATATGCTT 595
Db 2423 GGCAGAGGTGTTCCGGGCGGGGCATCTGCTGAGACCTGCACCTCGATATATGCTT 2482
Qy 596 CCTGCTGCCAGGTGGGCCCATCCCTGTTTAAAGGGTCCATGTTCCAGCTCAGCCAGTC 655
Db 2483 CCTGCTGCCAGGTGGGCCCATCCCTGTTTAAAGGGTCCATGTTCCAGCTCAGCCAGTC 2542
Qy 656 TGTCACTGCTTAATATGATGTCTGCGGAGGCTGAGTCTGAGTCCATTTACTTTGTAC 715
Db 2543 TGTCACTGCTTAATATGATGTCTGCGGAGGCTGAGTCTGAGTCCATTTACTTTGTAC 2602
Qy 716 ACAGTATGTTTAAACAAGAGCGACTTGGCCAAATCTCAGCGTGAAGAACTTCAGACAC 775
Db 2603 ACAGTATGTTTAAACAAGAGCGACTTGGCCAAATCTCAGCGTGAAGAACTTCAGACAC 2662
Qy 776 ATTGGGGTGAAGGCGCTGCTCACTGGGTCCAGCTCCCGCTCTGTTAGCCCAATGG 835
Db 2663 ATTGGGGTGAAGGCGCTGCTCACTGGGTCCAGCTCCCGCTCTGTTAGCCCAATGG 2722
Qy 836 GCTGCCGGGCTGGCGCGCACTTCTGTGTGCTGCCAAGTATGATGATCTCTGCTCCAC 895
Db 2723 GCTGCCGGGCTGGCGCGCACTTCTGTGTGCTGCCAAGTATGATGATCTCTGCTCCAC 2782
Qy 896 CTTGTGCTGTAAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 955
Db 2783 CTTGTGCTGTAAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2842
Qy 956 CCAAGTCTTAAGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1015
Db 2843 CCAAGTCTTAAGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2902
Qy 1016 CAGGAGGCGCAAGAGGGCTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 1074
Db 2903 CAGGAGGCGCAAGAGGGCTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 2962
Qy 1075 GGTCTCAGGGTTAACAGTACCTCTCAGTGTGAACACCTTGAAGAGGGTTTGGGAG 1134
Db 2963 GGTCTCAGGGTTAACAGTACCTCTCAGTGTGAACACCTTGAAGAGGGTTTGGGAG 3022
Qy 1135 CTGAATTAATCTAGTCACTGCTTCCATCTCTAAGCCCTTAACTGACCTTGTGTT 1194
Db 3023 CTGAATTAATCTAGTCACTGCTTCCATCTCTAAGCCCTTAACTGACCTTGTGTT 3082
Qy 1195 AATGTAGCTCTTGAATGAGAGTTTCTAAGATTAACACCTTCCATGAGGATTTGAACATA 1254
Db 3083 AATGTAGCTCTTGAATGAGAGTTTCTAAGATTAACACCTTCCATGAGGATTTGAACATA 3142

1255 TGAAGTTATTTGTAGGGAGAGTCTGAGGGGCAACACAGAGAGCCAGTCCCTCA 1314
1314 TGAAGTTATTTGTAGGGAGAGTCTGAGGGGCAACACAGAGAGCCAGTCCCTCA 3202
1315 GCCCAGAGACTGTCTTTTGTGATGACACCCCTCTTAACCTTTATGAGATGTGAC 1374
1374 GCCCAGAGACTGTCTTTTGTGATGACACCCCTCTTAACCTTTATGAGATGTGAC 3261
1375 TGTGTGCTCTTCTGTTGCAATCAGAGACACAGGATTTAAATATTATTTATT 1434
1434 TGTGTGCTCTTCTGTTGCAATCAGAGACACAGGATTTAAATATTATTTATT 3321
1435 TAAAGAGAGAGAGAGAGAGTCTGAGGGGCAACACAGAGAGCCAGTCCCTCA 1494
1494 TAAAGAGAGAGAGAGAGTCTGAGGGGCAACACAGAGAGCCAGTCCCTCA 3381
1495 GGGTGGGGGATCCCAACATCAGTCCCTGAGAGAGTGTGATTTGGGCTGATTTG 1554
1554 GGGTGGGGGATCCCAACATCAGTCCCTGAGAGAGTGTGATTTGGGCTGATTTG 3441
1555 CAGAAATCTTCTTCTGCTGGGCTGTGGCCCTCCCAATGCTTAACTTGGAA 1614
1614 CAGAAATCTTCTTCTGCTGGGCTGTGGCCCTCCCAATGCTTAACTTGGAA 3501
1615 TTCTACTATCCCAATGATTAATTCCTGTTTACCAAGTTAGGCTGTGAAGA 1674
1674 TTCTACTATCCCAATGATTAATTCCTGTTTACCAAGTTAGGCTGTGAAGA 3561
1675 AGGTAGAGGGTGGGCTTCAAGTCTCAAGGCTTCCCTTACCAAGGCTTCTTGGCC 1734
1734 AGGTAGAGGGTGGGCTTCAAGTCTCAAGGCTTCCCTTACCAAGGCTTCTTGGCC 3621
1735 CAGCTGTGTTCCCTCCTTCACTCCCTCTAATCTCTGAGAGCTGGGCTGATGAAG 1794
1794 CAGCTGTGTTCCCTCCTTCACTCCCTCTAATCTCTGAGAGCTGGGCTGATGAAG 3681
1795 CAGCTGTGTTCCCTCCTTCACTCCCTCTAATCTCTGAGAGCTGGGCTGATGAAG 1854
1854 CAGCTGTGTTCCCTCCTTCACTCCCTCTAATCTCTGAGAGCTGGGCTGATGAAG 3741
1855 CCACAACTCTGTTTGAAGTCTGACAGACAGAGAGCAAGAGGCTTCCCAAGCT 1914
1914 CCACAACTCTGTTTGAAGTCTGACAGACAGAGAGCAAGAGGCTTCCCAAGCT 3801
1915 TTGTCCATCTCAGCCCTCAGAGTATCTGTGCTTGGGATCTCACAAGAACTCAG 1974
1974 TTGTCCATCTCAGCCCTCAGAGTATCTGTGCTTGGGATCTCACAAGAACTCAG 3861
1975 AGCAGCCCTGCTGAGCTTGAAGAGTCTTATCTTCAAGGGGGTTTAACTGCGCTT 2034
2034 AGCAGCCCTGCTGAGCTTGAAGAGTCTTATCTTCAAGGGGGTTTAACTGCGCTT 3921
2035 GCAATATCTGCTTATTTTATGAGGGGAGATTTTATCTGTAAGTGAAGCATC 2094
2094 GCAATATCTGCTTATTTTATGAGGGGAGATTTTATCTGTAAGTGAAGCATC 3981
2095 AGAGTAAATGTTTATGAGCAAAATTAAGGCTTCTTATATGTTTA 2143
2143 AGAGTAAATGTTTATGAGCAAAATTAAGGCTTCTTATATGTTTA 3982
3982 AGAGTAAATGTTTATGAGCAAAATTAAGGCTTCTTATATGTTTA 4030

RESULT 14
ARS64090 4034 bp DNA linear PAT 08-OCT-2004
LOCUS ARS64090
DEFINITION Sequence 704 from patent US 6759515.
ACCESSION ARS64090
VERSION ARS64090.1 GI:53979141
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4034)

AUTHORS Xu J., Dillon D.C., Mitcham J.L., Harlocker S.L., Jiang Y.,
Kales M.D., Fanger G.R., Retter M.W., Stoik J.A., Day C.H.,
Vedick T.S., Carter D., Li S.X., Wang A., Skelly Y.A.W.,
Hedley M.T. and Henderson R.A.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: US 6759515-A 704 06-JUL-2004;
FEATURES
SOURCE Location/Qualifiers
1..4034
/organism="unknown"
/mol_type="genomic DNA"

Query Match 83.8%; Score 1796; DB 6; Length 4034;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2086; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

1943 AGGCTTGGAGTGGGAGGCTGGGCTGTTCTGAGAGTGGGCTGCTGCTTCTTC 115
1943 AGGCTTGGAGTGGGAGGCTGGGCTGTTCTGAGAGTGGGCTGCTGCTTCTTC 2002
116 TGTGATGAGACCGGCTGTGACAGATTCGCACTGAGAGTCTATTTGGCAGTGT 175
2003 TGTGATGAGACCGGCTGTGACAGATTCGCACTGAGAGTCTATTTGGCAGTGT 2062
176 GGCAGCTTCCCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 235
2063 GGCAGCTTCCCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2122
236 AGCTTCAAGCGGCTTCAAGCGGCTTCAAGCGGCTTCAAGCGGCTTCAAGCGGCT 295
2123 AGCTTCAAGCGGCTTCAAGCGGCTTCAAGCGGCTTCAAGCGGCTTCAAGCGGCT 2182
296 GGCCTTCCCTTCAAGCGGCTTCAAGCGGCTTCAAGCGGCTTCAAGCGGCTTCAAG 355
2183 GGCCTTCCCTTCAAGCGGCTTCAAGCGGCTTCAAGCGGCTTCAAGCGGCTTCAAG 2242
356 AGCTTCAAGCGGCTTCAAGCGGCTTCAAGCGGCTTCAAGCGGCTTCAAGCGGCT 415
2243 AGCTTCAAGCGGCTTCAAGCGGCTTCAAGCGGCTTCAAGCGGCTTCAAGCGGCT 2302
416 TCCCTTCCCTTCAAGCGGCTTCAAGCGGCTTCAAGCGGCTTCAAGCGGCTTCAAG 475
2303 TCCCTTCCCTTCAAGCGGCTTCAAGCGGCTTCAAGCGGCTTCAAGCGGCTTCAAG 2362
476 GCTTCTGCGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 535
2363 GCTTCTGCGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2422
536 GGCAGGCTGCTTCCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 595
2423 GGCAGGCTGCTTCCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2482
596 CCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 655
2483 CCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2542
656 TGTCACTGCTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 715
2543 TGTCACTGCTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2602
716 ACGAGTATTTTGAAGAGGCTTGGCCAAATCTCAGGTGAGAAATCTTCCAGCAG 775
2603 ACGAGTATTTTGAAGAGGCTTGGCCAAATCTCAGGTGAGAAATCTTCCAGCAG 2662
776 ATTGGAGTGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 835
2663 ATTGGAGTGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2722
836 GCTGCGGGCTGCGCGCAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 895
2723 GCTGCGGGCTGCGCGCAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2782

QY 536 GGCCAGGGGTTTCCGGGCGGGGGCATCTGCTGGACTTCGCCATCTGGATAGTCCCTT 595
 Db 2423 GGCCAGGGGTTTCCGGGCGGGGGCATCTGCTGGACTTCGCCATCTGGATAGTCCCTT 2482
 QY 536 CCTGCTGCCAGTGGGCCCATCCCTGTTTATGGGCTCCATTTGTCAGACTCAGCCAGTC 655
 Db 2483 CCTGCTGCCAGTGGGCCCATCCCTGTTTATGGGCTCCATTTGTCAGACTCAGCCAGTC 2542
 QY 656 TGTCACTGCTTATATGTTGTTGCGCGCAGAGGCTGGGCTGTGTGGCATTACTTTGCTAC 715
 Db 2543 TGTCACTGCTTATATGTTGTTGCGCGCAGAGGCTGGGCTGTGTGGCATTACTTTGCTAC 2602
 QY 716 ACAGGATGATTGACAAAGGAGCTTGGCCAAATATCAGGCTAGAAAATTCCAGCAC 775
 Db 2603 ACAGGATGATTGACAAAGGAGCTTGGCCAAATATCAGGCTAGAAAATTCCAGCAC 2662
 QY 776 ATTGGGGTGGAGGGGCTGCTCCTCAGTGGGTCAGAGCTCCCGCTCCTGTTAGCCCATGGG 835
 Db 2663 ATTGGGGTGGAGGGGCTGCTCCTCAGTGGGTCAGAGCTCCCGCTCCTGTTAGCCCATGGG 2722
 QY 836 GCTGCCGGGCTGGCGCCAGTTTCTGTTGCTGCGCAAAATATGTTGCTGTGCTGCGCAC 895
 Db 2723 GCTGCCGGGCTGGCGCCAGTTTCTGTTGCTGCGCAAAATATGTTGCTGTGCTGCGCAC 2782
 QY 896 CCTGCTGCTGAGGTCGTAGCTGACAGCTGGGGGCTGGGGGCTCCTCTCTCTCTC 955
 Db 2783 CCTGCTGCTGAGGTCGTAGCTGACAGCTGGGGGCTGGGGGCTCCTCTCTCTCTC 2842
 QY 956 CCCAGTCTCTAGGGGCTGCTGACTGAGAGGCTTCCAAAGGGGTTTCACTGGAATTATA 1015
 Db 2843 CCCAGTCTCTAGGGGCTGCTGACTGAGAGGCTTCCAAAGGGGTTTCACTGGAATTATA 2902
 QY 1016 CAGGGAGGCTCAGAAAGGGCTCCATGCACTGGAATGC- GSGACTCTGCAAGGTGATTA 1074
 Db 2903 CAGGGAGGCTCAGAAAGGGCTCCATGCACTGGAATGC- GSGACTCTGCAAGGTGATTA 2962
 QY 1075 GGGCTCAGGGTTAAACGTAGCCCTCCTAGTTGAGACACACTGTAAGAAAGGTTTTGGAG 1134
 Db 2963 GGGCTCAGGGTTAAACGTAGCCCTCCTAGTTGAGACACACTGTAAGAAAGGTTTTGGAG 3022
 QY 1135 CTGAATTAACCTCAGTCACTGCTGTTTCCATCTTAAGCCCTTAACCTGCACTTGCTT 1194
 Db 3023 CTGAATTAACCTCAGTCACTGCTGTTTCCATCTTAAGCCCTTAACCTGCACTTGCTT 3082
 QY 1195 AATGTAGCTCTTGCAATGGAGTTTCTAGAGTAAACACTCTTCATGGGATTTGAACATA 1254
 Db 3083 AATGTAGCTCTTGCAATGGAGTTTCTAGAGTAAACACTCTTCATGGGATTTGAACATA 3142
 QY 1255 TGAAGTTATTTGTAGGGGGAAGATCCTGAGGGGCAACACAGAACAGAGTCCCTCA 1314
 Db 3143 TGAAGTTATTTGTAGGGGGAAGATCCTGAGGGGCAACACAGAACAGAGTCCCTCA 3202
 QY 1315 GCCCAGAGCACTGCTTTTGTGATCAACCCCTCTTACCTTTTATCAGAGTGGCC 1374
 Db 3203 GCCCAGAGCACTGCTTTTGTGATCAACCCCTCTTACCTTTTATCAGAGTGGCC 3261
 QY 1375 TGTGTCCTTCTGTTGCTCACAAGAGACAGAGCATTTAAATTTAACTTATTTAT 1434
 Db 3262 TGTGTCCTTCTGTTGCTCACAAGAGACAGAGCATTTAAATTTAACTTATTTAT 3321
 QY 1435 TAACAAGTAAAGGAAATCCATTGCTAGCTTTTCTGTGTGGGTCTTAATTTGGGTA 1494
 Db 3322 TAACAAGTAAAGGAAATCCATTGCTAGCTTTTCTGTGTGGGTCTTAATTTGGGTA 3381
 QY 1495 GGGTGGGGGATCCCAACATCAGGTCCCTGAGATAGTGTCAATGGGCTGATCATTTG 1554
 Db 3382 GGGTGGGGGATCCCAACATCAGGTCCCTGAGATAGTGTCAATGGGCTGATCATTTG 3441
 QY 1555 CCAGATCTTCTTCTGCTGGGGTCTGGCCCCCAAAATGCTTAACCCAGAGCTTTGAAA 1614
 Db 3442 CCAGATCTTCTTCTGCTGGGGTCTGGCCCCCAAAATGCTTAACCCAGAGCTTTGAAA 3501

QY 1615 TTCTACTCATCCCAATGATTAATCCAAATGCTGTTTACCAAGGTTAGGGTGTGAAGA 1674
 Db 3502 TTCTACTCATCCCAATGATTAATCCAAATGCTGTTTACCAAGGTTAGGGTGTGAAGA 3561
 QY 1675 AGGTAGAGGGTGGGCTTCAGGCTCAACGAGCTTCCCTTAACCAACCTCTCTGTTGGCC 1734
 Db 3562 AGGTAGAGGGTGGGCTTCAGGCTCAACGAGCTTCCCTTAACCAACCTCTCTGTTGGCC 3621
 QY 1735 CAGCTGTTTCCCCCACTTCCATCCCTCTACTCTCTCTAGAACCTGGGCTGATGAAG 1794
 Db 3622 CAGCTGTTTCCCCCACTTCCATCCCTCTACTCTCTCTAGAACCTGGGCTGATGAAG 3681
 QY 1795 CACTGCCCAAAATTTCCCTTACCCCACTTTCCCTTACCCCACTTTCCCAACAGCT 1854
 Db 3682 CACTGCCCAAAATTTCCCTTACCCCACTTTCCCTTACCCCACTTTCCCAACAGCT 3741
 QY 1855 CCACAACCTGTTTGGAGCTACTGAGAGACAGAGACAAAGTCCGTTTCCCAAGCT 1914
 Db 3742 CCACAACCTGTTTGGAGCTACTGAGAGACAGAGACAAAGTCCGTTTCCCAAGCT 3801
 QY 1915 TTGTCACTCAGCCCCCAGAGTATATCTGCTTGGGGAATCTCAACAGAACTCAGG 1974
 Db 3802 TTGTCACTCAGCCCCCAGAGTATATCTGCTTGGGGAATCTCAACAGAACTCAGG 3861
 QY 1975 AGCAGCCCTGCTGAGCTAAGGAGGCTTATCTCTCAGAGGGGGTTTAAAGTCGCTT 2034
 Db 3862 AGCAGCCCTGCTGAGCTAAGGAGGCTTATCTCTCAGAGGGGGTTTAAAGTCGCTT 3921
 QY 2035 GCATATATGCTCTTATTTTATTTTATAGCGGGGTAATTTTATCTGTAAGTGAATC 2094
 Db 3922 GCATATATGCTCTTATTTTATTTTATAGCGGGGTAATTTTATCTGTAAGTGAATC 3981
 QY 2095 AGAGTATATGTTTATGTTGACAAATTAAGGCTTTCTTATATGTTTA 2143
 Db 3982 AGAGTATATGTTTATGTTGACAAATTAAGGCTTTCTTATATGTTTA 4030

Search completed: February 8, 2005, 17:33:36
 Job time : 9236.62 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 8, 2005, 11:26:32 / Search time 6982.34 Seconds
(without alignments)
11682.581 Million cell updates/sec

Title: US-09-841-894A-15

Perfect score: 2143
Sequence: 1 ACCAGGCGCTGCCAGAGCT.....AAGCTTCTATATGTTTA 2143

Scoring table: ~~GOLDBLUG~~
Gapop 60.0 / Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: gb_ests1:*
2: gb_ests2:*
3: gb_hic:*
4: gb_ests3:*
5: gb_ests4:*
6: gb_ests5:*
7: gb_ests6:*
8: gb_gsest1:*
9: gb_gsest2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1916	89.4	2477	3 HSM804244	AL832933 Homo sapi
2	704	32.9	1626	9 AY407706	AY407706 Homo sapi
3	648	30.2	897	6 CA489628	CA489628 AGENCOURT
4	617	28.8	916	5 BQ950912	BQ950912 AGENCOURT
5	602	28.1	651	6 CB048223	CB048223 NISC_g103
6	601	28.0	722	7 CN373215	CN373215 17005332
7	593	27.7	670	5 BU689021	BU689021 UI-CR-ECL
8	564	26.3	959	5 BQ950805	BQ950805 AGENCOURT
9	541	25.2	718	2 BE867241	BE867241 601442309
10	538	25.1	1025	2 BM915082	BM915082 AGENCOURT
11	528	24.6	581	7 CN373214	CN373214 170005321
12	491	22.9	589	4 BG469586	BG469586 602533622
13	475	22.2	875	5 BQ942028	BQ942028 AGENCOURT
14	474	22.1	1060	5 BM914562	BM914562 AGENCOURT
15	459	21.4	515	5 BX098291	BX098291 BX098291
16	430	20.1	437	7 CF135166	CF135166 UI-HF-CB0
17	429	20.0	734	6 CD634718	CD634718 56050152J
18	390	18.2	418	2 BF922235	BF922235 OV2-NT014
19	382	17.8	1667	5 BM912193	BM912193 AGENCOURT
20	378	17.6	740	6 CD634716	CD634716 560501440
21	377	17.6	494	4 CF134970	CF134970 UI-HF-CB0
22	373	17.4	850	4 BF972601	BF972601 602243025
23	347	16.2	412	2 AM175665	AM175665 RC3-BT004
24	339	15.8	599	6 CB050165	CB050165 NISC_gj15

c 25	323	15.1	410	6	CD634731	CD634731 56088181H
c 26	323	15.1	413	6	CD634732	CD634732 56088181H
c 27	323	15.1	756	6	CD634730	CD634730 56088057J
c 28	319	14.9	448	2	BE674096	BE674096 7d74g04.x
c 29	300	14.0	800	4	BG469487	BG469487 602532993
c 30	300	14.0	894	4	BG469520	BG469520 602532833
c 31	299	14.0	491	1	AA631143	AA631143 ng75g08..s
c 32	293	13.7	313	6	CB050330	CB050330 NISC_gj16
c 33	283	13.2	737	6	CD634720	CD634720 56050126J
c 34	282	13.2	586	5	BP326798	BP326798 BP326798
c 35	281	13.1	469	1	AI703348	AI703348 wd93b09..x
c 36	275	12.8	1450	9	AY407707	AY407707 Pan trogl
c 37	270	12.6	325	2	BE673709	BE673709 7d79g07.x
c 38	268	12.5	327	1	AI696920	AI696920 wq75c01.x
c 39	266	12.4	716	6	CD634717	CD634717 56050152H
c 40	265	12.4	435	6	CB049513	CB049513 NISC_gj11
c 41	264	12.3	320	2	BF222329	BF222329 TP51C08..x
c 42	263	12.3	315	1	AA640153	AA640153 np28B03..s
c 43	261	12.2	320	2	BF223843	BF223843 7G80B09..x
c 44	260	12.1	313	1	AI587483	AI587483 t51c10.x
c 45	255	11.9	306	1	AA631024	AA631024 ng75g11..s

ALIGNMENTS

RESULT 1
HSM804244
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 2477)
Ansoerge,W., Krieger,S., Regiert,T., Rittmueller,C., Schwager,B.,
Mewes,H.W., Well,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
Wiemann,S.
The German cDNA Consortium
Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKFZp666D0110) is available at the RZPD Deutsches
Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp666D0110
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
Location/Qualifiers
1..2477
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="RZPD:DKFZp666D0110"
/db_xref="taxon:9606"
/clone="DKFZp666D0110"
/tissue_type="stomach"
/clone_lib="666 (synonym: hato2). Vector pSport1; host
DH10B; sites NotI + SalI"
/dev_stage="adult"
/note="proteins, alternative start, differentially
spliced"
1..2477
/gene="DKFZp666D0110"
370..1065
/gene="DKFZp666D0110"

QY	2036	CAATTAATGCGCTTAATTTTATTTAGCGGGGCAATATTTTATTTACGTAGAGCAATCA	2095
Db	2341	CAATTAATGCGCTTAATTTATTTATTTAGCGGGGCAATATTTTATTTACGTAGAGCAATCA	24000
QY	2096	GAGTAAATGTTTATGTGTGACAAATTAAGGCTTTCTTATATGTTTA	2143
Db	2401	GAGTAAATGTTTATGTGTGACAAATTAAGGCTTTCTTATATGTTTA	2448
RESULT 2			
LOCUS	AY407706	1626 bp	DNA
DEFINITION	Homo sapiens HCM2980 gene, VIRTUAL TRANSCRIPT, partial sequence,		linear GSS 12-DEC-2003
ACCESSION	AY407706		
VERSION	AY407706.1		
KEYWORDS	GSS.		
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 1626)		
AUTHORS	Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene clones		
JOURNAL	Science 302 (5652), 1960-1963 (2003)		
PUBMED	14671302		
REFERENCE	2 (bases 1 to 1626)		
AUTHORS	Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Direct Submision		
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.		
FEATURES			
source	1..1626		
	/organism="Homo sapiens"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:9606"		
gene	<1..>1626		
	/locus_tag="HCM2980"		
ORIGIN			
Query Match	32.9%: Score 704; DB 9; Length 1626;		
Best Local Similarity	100.0%: Pred. No. 0;		
Matches 704; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
QY	58	GCGTTCGATGGGCGACCTGGGCGCTGTTCTGCACTGGCCATCTCCCTGATCTTCTC	117
Db	923	GCGTTCGATGGGCGACCTGGGCGCTGTTCTGCACTGGCCATCTCCCTGATCTTCTC	982
QY	118	TGTCATAGACCCGCTGCTGTGACGACATTCGGGACCTCAGGACGTCTATTTGGCAGTGTG	177
Db	983	TGTCATAGACCCGCTGCTGTGACGACATTCGGGACCTCAGGACGTCTATTTGGCAGTGTG	1042
QY	178	CAGCTTTCCTCTGTGCTGCTCCGGTGGCAATGCGCTGTCCACAGTGTGGCCGTGTGACAG	237
Db	1043	CAGCTTTCCTCTGTGCTGCTCCGGTGGCAATGCGCTGTCTCCACAGTGTGGCCGTGTGACAG	1102
QY	238	CTTACGCGCCCTCAACGGGATTACCTTCTAGCCCTGCAATCTGCTCTTACACACTGG	297
Db	1103	CTTACGCGCCCTCAACGGGATTACCTTCTAGCCCTGCAATCTGCTCTTACACACTGG	1162
QY	298	CCTCCCTCTACCAACGGGAGAAAGCAGGAGTTCCTGSCCAATTAACGAGGGGACACTGGAG	357
Db	1163	CCTCCCTCTACCAACGGGAGAAAGCAGGAGTTCCTGSCCAATTAACGAGGGGACACTGGAG	1222

FEATURES	source
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
ORGANISM	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
ORGANISM	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
ORGANISM	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
ORGANISM	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
ORGANISM	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
ORGANISM	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
ORGANISM	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
ORGANISM	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
ORGANISM	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
ORGANISM	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
ORGANISM	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
ORGANISM	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
ORGANISM	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
ORGANISM	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
ORGANISM	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
ORGANISM	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	

ORIGIN
cancer genes encoding membrane and secreted proteins.
Manuscript submitted."

Query Match 30.2%; Score 648; DB 6; Length 897;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ACCAGGGGGTGGCCAGAGCTGAGCCGGGACCCGAGGACCTATGATGAAGCG 60
DB 11 ACCAGGGGGTGGCCAGAGCTGAGCCGGGACCCGAGGACCTATGATGAAGCG 70
QY 61 TTGGATGGAGAGCTGGGGCTGTTCTCGAGTGGCCATCTCCGATCTTCTCTG 120
DB 71 TTGGATGGAGAGCTGGGGCTGTTCTCGAGTGGCCATCTCCGATCTTCTCTG 130
QY 121 TCATGAGACCGGCTGTGTGAGAGATTCGGCACTGAGAGTCTATTGAGGAG 180
DB 131 TCATGAGACCGGCTGTGTGAGAGATTCGGCACTGAGAGTCTATTGAGGAG 190
QY 181 CTTTCCCTGTGGCTGGGTCGACATGCTGTCGACAGTGGCCGCTGTGACAGCTT 240
DB 191 CTTTCCCTGTGGCTGGGTCGACATGCTGTCGACAGTGGCCGCTGTGACAGCTT 250
QY 241 CAGCGCCCTTCAACCGGGTTCACCTTCTCAGCCCTGAGATCTGCTTACACTG 300
DB 251 CAGCGCCCTTCAACCGGGTTCACCTTCTCAGCCCTGAGATCTGCTTACACTG 310
QY 301 CCGCTTCAACCGGGGAGAGAGGTTCTCTGCTCCAAATACCGAGGGAGACATG 360
DB 311 CCGCTTCAACCGGGGAGAGAGGTTCTCTGCTCCAAATACCGAGGGAGACATG 370
QY 361 CTAGCACTGAGAGACAGCTGATGACAGCTTCTGCGAGGCTTAAAGCTGAGCT 420
DB 371 CTAGCACTGAGAGACAGCTGATGACAGCTTCTGCGAGGCTTAAAGCTGAGCT 430
QY 421 TTCCCTATGAGACAGTGGGCTGTGAGAGGAGGAGGCTGCTTCCACTTCAAC 480
DB 431 TTCCCTATGAGACAGTGGGCTGTGAGAGGAGGAGGCTGCTTCCACTTCAAC 490
QY 481 GCGGGGCTCTGCTGTGATGTCTCCGTAAGTGGGAGGAGGAGGAGGAGGAG 540
DB 491 GCGGGGCTCTGCTGTGATGTCTCCGTAAGTGGGAGGAGGAGGAGGAGGAG 550
QY 541 GGGTGTTCGGGCGGGGATCTGCTGAGACCTGCGCACTCGATGATGCTTCT 600
DB 551 GGGTGTTCGGGCGGGGATCTGCTGAGACCTGCGCACTCGATGATGCTTCT 610
QY 601 TGTCCAGAGTGGCCCATCTCTTTATGAGGCTTCAATGCTTCAAGCTCA 648
DB 611 TGTCCAGAGTGGCCCATCTCTTTATGAGGCTTCAATGCTTCAAGCTCA 658

RESULT 4
BO950912 916 bp mRNA linear EST 21-AUG-2002
LOCUS BO950912
DEFINITION AGENOURT 8754471 Lupski sciatic nerve Homo sapiens cDNA clone
IMAGE:6205362 5', mRNA sequence.
ACCESSION BO950912
VERSION BO950912.1 GI:22366390
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.

FEATURES
source
1..916
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6205362"
/sex="male"
/tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
/clone_id="Lupski_sciatic_nerve"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TGACCCACGAGGTCG-3' and
5'-GACTAGTCTGATGCGAGGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

ORIGIN

Query Match 28.8%; Score 617; DB 5; Length 916;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 617; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1092 TAGCTCTAGTGAACACACTAGAGAGGTTTGGAGCTGAATTAACAGTCA 1151
DB 1 TAGCTCTAGTGAACACACTAGAGAGGTTTGGAGCTGAATTAACAGTCA 60
QY 1152 CTTGTTTCCATCTCTTAAGCCCTTAACCTGACGCTTCTTTAAGTACCTTGCATG 1211
DB 61 CTTGTTTCCATCTCTTAAGCCCTTAACCTGACGCTTCTTTAAGTACCTTGCATG 120
QY 1212 GGAATTTCTAGATGAACACTCTCTCATGGGATTTGAACATTAAGTATTGAG 1271
DB 121 GGAATTTCTAGATGAACACTCTCTCATGGGATTTGAACATTAAGTATTGAG 180
QY 1272 GGAAGAGCTCTGAGGGGCAACAAAGAACAGTCCCTCAGCCACAGACTGT 1331
DB 181 GGAAGAGCTCTGAGGGGCAACAAAGAACAGTCCCTCAGCCACAGACTGT 240
QY 1332 TTTCGATCAACCCCTCTTAACCTTTATGAGATGTGGCTGTGCTTCTGTTG 1391
DB 241 TTTCGATCAACCCCTCTTAACCTTTATGAGATGTGGCTGTGCTTCTGTTG 300
QY 1392 CCATCAGAGACAGAGCATTTAATATTATTAATTAATTAATTAATTAATTA 1451
DB 301 CCATCAGAGACAGAGCATTTAATATTATTAATTAATTAATTAATTAATTA 360
QY 1452 ATCCATTTGCTAGCTTTCTGTGTGGTGTCTAATATTGGGAGGAGATCCCA 1511
DB 361 ATCCATTTGCTAGCTTTCTGTGTGGTGTCTAATATTGGGAGGAGATCCCA 420
QY 1512 CAATCAGGTCCTCTGAGATGCTGATCATTTGGGCTGATATGCGAGATCTTCT 1571
DB 421 CAATCAGGTCCTCTGAGATGCTGATCATTTGGGCTGATATGCGAGATCTTCT 480
QY 1572 TGGGGTCTGGCCCCCAAAATGCTTAACCCAGAGCTTGAATTTCTATCCCAAT 1631
DB 481 TGGGGTCTGGCCCCCAAAATGCTTAACCCAGAGCTTGAATTTCTATCCCAAT 540
QY 1632 GATTAATTCAAATATGCTTTAACCAGGTTAGGCTGTGAAGAGAGTGAAGGCT 1691
DB 541 GATTAATTCAAATATGCTTTAACCAGGTTAGGCTGTGAAGAGAGTGAAGGCT 600


```

QY 751 ACTCAGCGTGAAGAACTTCACAGACATTGGGGTGGAGGGCTGCTCCTCAGTGGTCCAGC 810
Db 1 ACTCAGCGTGAAGAACTTCACAGACATTGGGGTGGAGGGCTGCTCCTCAGTGGTCCAGC 60
QY 811 TCCCGCTCTCTGTTAGCCCAATGGGGCTGGCGGGCTGGCCGCACTTCTCTGCTGCTCA 870
Db 61 TCCCGCTCTCTGTTAGCCCAATGGGGCTGGCGGGCTGGCCGCACTTCTCTGCTGCTCA 120
QY 871 AAGTAATGTGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 930
Db 121 AAGTAATGTGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 931 GGGTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 990
Db 181 GGGTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 991 AAGGGGGTTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1050
Db 241 AAGGGGGTTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 1051 -GGGAGCTGAGAGTGAATTCACAGGCTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1109
Db 301 GGGAGCTGAGAGTGAATTCACAGGCTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 1110 AACCTTGAAGAGGGGTTTGGAGCTGAATTAACCTGCTGCTGCTGCTGCTGCTGCTG 1169
Db 361 AACCTTGAAGAGGGGTTTGGAGCTGAATTAACCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 1170 AGCCCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1229
Db 421 AGCCCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 1230 CACTCTCTCAATGGGATTTGAACATATGAAGTTATTTGAGGGAGAGTCTGAGAGG 1289
Db 481 CACTCTCTCAATGGGATTTGAACATATGAAGTTATTTGAGGGAGAGTCTGAGAGG 540
QY 1290 AACACACAGAGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1349
Db 541 AACACACAGAGACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 1350 TCTTACCTTTTATCAGAGATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1409
Db 601 TCTTACCTTTTATCAGAGATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 1410 CATTAAATATTTAATTATTTATTTAACAAGTAGAAGGAATCATTGCTAGCTTTTC 1469
Db 661 CATTAAATATTTAATTATTTATTTAACAAGTAGAAGGAATCATTGCTAGCTTTTC 720
QY 1470 TG 1471
Db 721 TG 722

```

```

RESULT 7
LOCUS BU689021/c 670 bp mRNA linear EST 07-OCT-2002
DEFINITION UI-CF-EC1-ady-f-04-0-UI-s1 UI-CF-EC1 Homo sapiens cDNA clone
VERSION BU689021
ACCESSION BU689021 GI:23546376
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 670)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLES Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PubMed 8889548

```

COMMENT

Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul.mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.researchgen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this cDNA
sequence: 1-28, >AT rich#low_complexity
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES

source

Location/Qualifiers
1..670
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-EC1-ady-f-04-0-UI"
/tissue_type="Lung"
/dev_stage="Adult and Fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-EC1"
/note="Organ: Lung; Vector: pRTT3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-EC1 is a normalized cDNA library containing the
following tissue(s): Normal lung from adult and from fetal
day 64, day 87, week 19 and week 42. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pRTT3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dr)18 tail. The sequence tag for this library is
AAGTCTTAC.
TAG TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371
and 380-383
TAG_LIB=UI-CF-EC1
TAG_SEQ=AAGTCTTAC"

ORIGIN

Query Match 27.7%; Score 593; DB 5; Length 670;
Best Local Similarity 99.8%; Pred. No. 4,9e-309;
Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1500 GGGGATCCCAACATAGAGTCCCTGAGATAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1559
Db 661 GGGGATCCCAACATAGAGTCCCTGAGATAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 602
QY 1560 ATCTTCTTCCCTGGGGCTGGCCCCCAAAAGCCCTAACCAGACCTTGGAAATTTCTA 1619
Db 601 ATCTTCTTCCCTGGGGCTGGCCCCCAAAAGCCCTAACCAGACCTTGGAAATTTCTA 542
QY 1620 CTCATCCCAATGATTAATTCATATGCTGTTACCAAGGTTAGGGTGTGAAGGAAGTTA 1679
Db 541 CTCATCCCAATGATTAATTCATATGCTGTTACCAAGGTTAGGGTGTGAAGGAAGTTA 482
QY 1680 GAGGGTGGGGCTTCAGGCTCAAGGCTTCCCTTAACCAACCCCTCTTCTTGGCCAGCC 1739
Db 481 GAGGGTGGGGCTTCAGGCTCAAGGCTTCCCTTAACCAACCCCTCTTCTTGGCCAGCC 422
QY 1740 TGGTCCCCCACTTCACTCCCTCTACTCTCTAGAGACTGGGCTGATGAAGGACACTG 1799
Db 421 TGGTCCCCCACTTCACTCCCTCTACTCTCTAGAGACTGGGCTGATGAAGGACACTG 362

Plate: L1AM9559 row: a column: 04
High quality sequence stop: 693.
Location/Qualifiers

FEATURES

source

1. 718
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3846411"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_65"
/note="Organ: colon; Vector: pCMV-Sport6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."

ORIGIN

Query Match 25.2%; Score 541; DB 2; Length 718;
Best Local Similarity 100.0%; Pred. No. 7.6e-281;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 116 TCTGTATGACCGGCTGTGACGATTCGCACTCGACGCTATTGGCCAGTGT 175
DB 1 TCTGTATGACCGGCTGTGACGATTCGCACTCGACGCTATTGGCCAGTGT 60
QY 176 GGCAGCTTTCCTGTGCTGCGGTGACACATGCTGTCCACAGTGTGCGGTGAC 235
DB 61 GGCAGCTTTCCTGTGCTGCGGTGACACATGCTGTCCACAGTGTGCGGTGAC 120
QY 236 AGCTTCAGCCGCTTCACCGGCTTCACTTCTCACTGCTGCTGCTGCTGCTGCT 295
DB 121 AGCTTCAGCCGCTTCACCGGCTTCACTTCTCACTGCTGCTGCTGCTGCTGCT 180
QY 296 GGCCTCCCTTACCAACCGGAGAGAGAGTTCCTGCGCCCAATACCGAGGAGCACTGG 355
DB 181 GGCCTCCCTTACCAACCGGAGAGAGAGTTCCTGCGCCCAATACCGAGGAGCACTGG 240
QY 356 AGGTGCTAGAGAGAGAGAGAGTTCCTGCGCCCAATACCGAGGAGCACTGGAGC 415
DB 241 AGGTGCTAGAGAGAGAGAGAGTTCCTGCGCCCAATACCGAGGAGCACTGGAGC 300
QY 416 TCCCTTCCCTAATGAGACAGTGTGCTGAGAGCACTGCTGCTGCTGCTGCTGCTG 475
DB 301 TCCCTTCCCTAATGAGACAGTGTGCTGAGAGCACTGCTGCTGCTGCTGCTGCTG 360
QY 476 GCTCTGCGGGGCTTGTGCTGATGCTCCGTAAGTGTGAGTGTGAGTGTGAGTGTG 535
DB 361 GCTCTGCGGGGCTTGTGCTGATGCTCCGTAAGTGTGAGTGTGAGTGTGAGTGTG 420
QY 536 GGCAGAGTGTGCTGCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 595
DB 421 GGCAGAGTGTGCTGCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 596 CTTGCTGTCCAGAGTGGCCCATCCCTGTTTATGAGCTCATTTGTCAGCTCAGCAATG 655
DB 481 CTTGCTGTCCAGAGTGGCCCATCCCTGTTTATGAGCTCATTTGTCAGCTCAGCAATG 540
QY 656 T 656
DB 541 T 541

```

RESULT 10
BM915082 1025 bp mRNA linear EST 12-MAR-2002
LOCUS DEFINITION
AGENCY 6702317 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5481218
5', mRNA sequence.
ACCESSION BM915082
VERSION BM915082.1 GI:19365461
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
1 (bases 1 to 1025)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLI)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNLI at:
<http://image.llnl.gov>
Plate: L1CM2005 row: f column: 03
High quality sequence start: 35
High quality sequence stop: 657.
High quality sequence

FEATURES

source

1. 1025
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5481218"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_41"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 25.1%; Score 538; DB 5; Length 1025;
Best Local Similarity 99.6%; Pred. No. 3.3e-279;
Matches 758; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

```

QY 615 CCATCCCTGTTTATGAGCTCATTGTCACCTCAGCAGCTGTCATGCTATATGATG 674
DB 12 CCATCCCTGTTTATGAGCTCATTGTCACCTCAGCAGCTGTCATGCTATATGATG 71
QY 675 TCTGCCGAGGCTGCGGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 724
DB 72 TCTGCCGAGGCTGCGGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 131
QY 735 AGCAGCTTGCCAAATCTCAGGCTAGAAATCTCCAGCATTTGGGCTGAGAGGCTG 794
DB 132 AGCAGCTTGCCAAATCTCAGGCTAGAAATCTCCAGCATTTGGGCTGAGAGGCTG 191
QY 795 CTCACTGGTCCGAGCTCCCGCTCTGTTAGCCCATGAGGAGCTGCGGCTGCGCCA 854
DB 192 CTCACTGGTCCGAGCTCCCGCTCTGTTAGCCCATGAGGAGCTGCGGCTGCGCCA 251
QY 855 GTTTCGTTGTCGCAAGTAATGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 914
DB 252 GTTTCGTTGTCGCAAGTAATGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 311
QY 915 TAAGTCAGAGCTGAGGAGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 974
DB 312 TAAGTCAGAGCTGAGGAGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 371
QY 975 TGAAGTGAAGCTTCCAGAGGAGTTCAGTCTGAGCTTATACAGGAGGAGGAGGCT 1034
DB 372 TGAAGTGAAGCTTCCAGAGGAGTTCAGTCTGAGCTTATACAGGAGGAGGAGGCT 431
QY 1035 CCATGCACTGAAATGC-GGGAATCTGCAAGTGAATTAACCAAGCTCAGAGGTTAA 1093
DB 432 CCATGCACTGAAATGC-GGGAATCTGCAAGTGAATTAACCAAGCTCAGAGGTTAA 491
QY 1094 GCCTCTAGTTAGACACACTAGAGAGGTTTGGAGCTGAATAACTCAATGATCACC 1153

```

```

Db      492 GCCTCAGTGAACACACCTAGAGAGGGTTTGGAGCTGAATTAACACGACAC 551
Qy      1154 TGGTTTCCCATCTTAAGCCCTTAACCTGACAGCTGTTTAATAGTACTGTCAGG 1213
Db      552 TGGTTTCCCATCTTAAGCCCTTAACCTGACAGCTGTTTAATAGTACTGTCAGG 611
Qy      1214 AGTTCTAGAGTAAACACTCTCCATGAGATTGAAACATATGAAGTTATTTGTAGGG 1273
Db      612 AGTTCTAGAGTAAACACTCTCCATGAGATTGAAACATATGAAGTTATTTGTAGGG 671
Qy      1274 AAGAGTCTGAGGGGCAACACAAAGAACAGGTCCTCAGGCCACAGACATGCTTTT 1333
Db      672 AAGAGTCTGAGGGGCAACACCAAGAACAGGTCCTCAGGCCACAGACATGCTTTT 731
Qy      1334 TGCTGATCACCCTCTTACCTTTATCAGAGATGAGCC 1374
Db      732 TGCTGATCACCCTCTTACCTTTATCAGAGATGAGCC 772

RESULT 11
LOCUS   CN373214          581 bp      mRNA      linear      EST 16-MAY-2004
DEFINITION 1700532189001 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN373214
VERSION   CN373214.1 GI:47373148
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 581)
AUTHORS  Brandenberger, R., Wei, H., Zhang, S., Lei, S., Muraige, J., Flisk, G.J.,
          Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M.S., Mandalam, R.,
          Lebowicki, J. and Stanton, L.W.
          Transcriptional characterization elucidates signaling networks that
          control human ES cell growth and differentiation
          Nat. Biotechnol. 22 (6), 707-716 (2004)
JOURNAL  Contact: Brandenberger R
COMMENT   Regenerative Medicine
          Geron Corporation
          230 Constitution Drive, Menlo Park, CA 94025, USA
          Tel: 650 473 8658
          Fax: 650 473 7760
          Email: rbrandenberger@geron.com
          Insert Length: 581 Std Error: 0.00.
FEATURES
         source
         1..581
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /tissue_type="embryonic stem cells, cell lines H1, H7, and
            H9"
            /clone_11b="GRN ES"
            /note="oligo dt primed, full-length enriched cDNA library
            from undifferentiated hES cell lines H1 (p32), H7 (p29),
            and H9 (p26) maintained in feeder-free conditions"
ORIGIN
Query Match 24.6%; Score 528; DB 7; Length 581;
Best Local Similarity 100.0%; Pred. No. 8,3e-274;
Matches 528; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1152 CCGTGTTCCTCACTTAAGCCCTTAACCTGACAGCTGTTTAATAGTACTGTCAGG 1211
Db      39 CCGTGTTCCTCACTTAAGCCCTTAACCTGACAGCTGTTTAATAGTACTGTCAGG 98
Qy      1212 GGAAGTTTCAAGATGAACACTCTCCATGAGATTGAAACATATGAAGTTATTTGTAGG 1271
Db      99 GGAAGTTTCAAGATGAACACTCTCCATGAGATTGAAACATATGAAGTTATTTGTAGG 158
Qy      1272 GGAAGATCTCTGAGGGGCAACACAAAGAACAGGTCCTCAGGCCACAGACATGCTTT 1331

```

```

Db      159 GGAAGATCTCTGAGGGGCAACACAAAGAACAGGTCCTCAGGCCACAGACATGCTTT 218
Qy      1332 TTGCTGATCAACCCCTCTTACCTTTATCAGAGATGAGGCTGTTGCTTCTGTTG 1391
Db      219 TTGCTGATCAACCCCTCTTACCTTTATCAGAGATGAGGCTGTTGCTTCTGTTG 278
Qy      1392 CCATCAACAGACACAGGATTTAAATATTAACTTATTATTAAACAAGTGAAGGGA 1451
Db      279 CCATCAACAGACACAGGATTTAAATATTAACTTATTATTAAACAAGTGAAGGGA 338
Qy      1452 ATCCATGCTACCTTTCTGTGTGGTGTCTAATATTGGGTAGGGTGGGGATCCCA 1511
Db      339 ATCCATGCTACCTTTCTGTGTGGTGTCTAATATTGGGTAGGGTGGGGATCCCA 398
Qy      1512 CAATCAGTCCCTGAGATAGCTGTGATTTGGGCTGATTCATTCGCAATCTTCTCC 1571
Db      399 CAATCAGTCCCTGAGATAGCTGTGATTTGGGCTGATTCATTCGCAATCTTCTCC 458
Qy      1572 TGGGGTCTGGCCCCCAAAATGCTTAACGACAGACCTTGAAATTTACTCATCCCAAT 1631
Db      459 TGGGGTCTGGCCCCCAAAATGCTTAACGACAGACCTTGAAATTTACTCATCCCAAT 518
Qy      1632 GATTAATCCAAATGCTGTACCAAGTTAGGGTGTGGAAGAGGTA 1679
Db      519 GATTAATCCAAATGCTGTACCAAGTTAGGGTGTGGAAGAGGTA 566

RESULT 12
LOCUS   BG469586          589 bp      mRNA      linear      EST 21-MAR-2001
DEFINITION 602533622F1 NIH_MGC_15 Homo sapiens cDNA IMAGE:4661500 5',
          mRNA sequence.
ACCESSION BG469586
VERSION   BG469586.1 GI:13401861
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 589)
AUTHORS  NIH-MGC http://mgs.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)
JOURNAL  Contract: Robert Strausberg, Ph.D.
          Email: cgabbs-remail.nih.gov
          Tissue Procurement: ATCC
          DNA Library Preparation: Ling Hong/Rubin Laboratory
          CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: NIH Intramural Sequencing Center
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: L1CM1460 row: k column: 05
          High quality sequence stop: 587.
FEATURES
         source
         1..589
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone_11b="IMAGE:4661500"
            /tissue_type="adenocarcinoma cell line"
            /lab_host="DH10B (phage-resistant)"
            /clone_11b="NIH MGC_15"
            /note="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2:
            EcoRI; cDNA made by oligo-dt priming. Directionally
            cloned into EcoRI/XhoI sites using the following 5'
            adaptor: GGCACGAG(G) Size-selected >500bp for average
            insert size 1.8kb. Library constructed by Ling Hong in
            the laboratory of Gerald M. Rubin (University of
            California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies)"
ORIGIN

```


Tissue Procurement: Dr. Mark Watson
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.jnl.gov>
 Plate: LNCM2002 row: m column: 14
 High quality sequence stop: 485.
 Location/Qualifiers
 1.1060
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5480245"
 /lab_host="DH10B (phage-resistant)"
 /clone_1ib="NIH MGC 113"
 /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; CDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the
 Laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN

Query Match 22.1%; Score 474; DB 5; Length 1060;
 Best Local Similarity 100.0%; Pred. No. 1.6e-244;
 Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 352 CTGGAGGTCTAGCACTAGAGACAGCTTATGACCGCTTCTGCGACGCGCTTAACCTG 411
DB 1 CTGGAGGTCTAGCACTAGAGACAGCTTATGACCGCTTCTGCGACGCGCTTAACCTG 60
QY 412 GAGCTCCCTCCCTAATGACAGCTGGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 471
DB 61 GAGCTCCCTCCCTAATGACAGCTGGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 472 CCGCGCTCTGCGGGGCTCTGCTGTGATGTCTCCGTACGTGTGTGTGTGTGTGTGTGTGT 531
DB 121 CCGCGCTCTGCGGGGCTCTGCTGTGATGTCTCCGTACGTGTGTGTGTGTGTGTGTGTGT 180
QY 532 CCGAGGCCAGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 591
DB 191 CCGAGGCCAGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
QY 592 CTTCTGCTGCTCCAGAGTGGCCCATCCCTGTTTATGAGGCTTCATTGTCAGCTACGCC 651
DB 241 CTTCTGCTGCTCCAGAGTGGCCCATCCCTGTTTATGAGGCTTCATTGTCAGCTACGCC 300
QY 652 AGTGTGTCACTGCTATATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 711
DB 301 AGTGTGTCACTGCTATATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
QY 712 CTACACAGGTAGTATTTGACAGAGGAGCTTGGCCAAATATCTAGAGGTGAAAACCTTCCA 771
DB 361 CTACACAGGTAGTATTTGACAGAGGAGCTTGGCCAAATATCTAGAGGTGAAAACCTTCCA 420
QY 772 GCACATTTGGGGTGAAGAGGCTGCTCACTGGGTCCCAAGTCCCGGCTCCCTGTTA 825
DB 421 GCACATTTGGGGTGAAGAGGCTGCTCACTGGGTCCCAAGTCCCGGCTCCCTGTTA 474

```

RESULT 15
 LOCUS BX098291 515 bp mRNA 1linear EST 04-FEB-2003
 DEFINITION BX098291 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
 IMAGE998P04693; IMAGE:308595, mRNA sequence.
 ACCESSION BX098291 GI:27843586
 VERSION EST.
 KEYWORDS Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 515)
 AUTHORS Ebert, L., Heil, O., Hennig, S., Neubert, P., Parsch, E., Peters, M.,
 Radloff, U., Schneider, D. and Korn, B.
 TITLE Human Unigeneset - RZPD3
 JOURNAL Unpublished (2003)
 COMMENT Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
 RZPD: IMAGE998P04693.
 RZPDLIB: I.M.A.G.E. cDNA Clone Collection;
 Human Unigeneset - RZPD3 (RZPDLIB No.972)
<http://www.rzpd.de/Clovecards/cgi-bin/showLib.pl.cgi?response?libNo=972> Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Heubnerweg 6, D-14059 Berlin, Germany
 Tel: +49 30 32639 101
 Fax: +49 30 32639 111
 www.rzpd.de

FEATURES

source

This clone is available royalty-free from RZPD;
 contact RZPD (clone@rzpd.de) for further information. Seq primer:
 M13r, Primer sequence: TTTACACAGAGAAACGATATGAC.
 Location/Qualifiers

```

1.515
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE998P04693; IMAGE:308595"
/def_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_1ib="Soares_fetal_lung_NbHL19W"
/note="Organ: lung; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG-3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Benito
Soares and M.Patino Bonaldo. This library was constructed
from the same fetus as the fetal heart library, Soares
fetal heart NbHL19W."

```

ORIGIN

Query Match 21.4%; Score 459; DB 5; Length 515;
 Best Local Similarity 100.0%; Pred. No. 2.1e-236;
 Matches 459; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1596 TAACCCAGAGCTTGAATTTCTACTATCCCAATGATTAATTCAGGCTTACCCA 1655
DB 34 TAACCCAGAGCTTGAATTTCTACTATCCCAATGATTAATTCAGGCTTACCCA 93
QY 1656 AGGTTAGGGTGTGAAGAGAGTGAAGGGTGGGCTTCAAGGTCTCAAGGCTTCCCTAAC 1715
DB 94 AGGTTAGGGTGTGAAGAGAGTGAAGGGTGGGCTTCAAGGTCTCAAGGCTTCCCTAAC 153
QY 1716 CACCCCTCTTCTTTGGCCAGGCTGGTCCGCCCACTTCCACTCCCTCTACTCTCTG 1775
DB 154 CACCCCTCTTCTTTGGCCAGGCTGGTCCGCCCACTTCCACTCCCTCTACTCTCTG 213
QY 1776 AGGACTGGGCTGATGAAGCACTGCCCAAAATTTCCCTACCCCACTTCCCTACCC 1835
DB 214 AGGACTGGGCTGATGAAGCACTGCCCAAAATTTCCCTACCCCACTTCCCTACCC 273
QY 1836 CCAACTTTTCCCAACAGCTCCCAACACCTGTTTGAAGCTATCTGCAAGAGACCAAGAGCA 1895
DB 274 CCAACTTTTCCCAACAGCTCCCAACACCTGTTTGAAGCTATCTGCAAGAGACCAAGAGCA 333
QY 1896 AGTGCGTTTCCCAAGCTTTTGCATCTCAGCCCAAGAGATATCTGTGCTGGAGAA 1955

```

```
Db      334 AGTGGGTTTCCCAAGCCTTTGTCAATCTCAGCCCCCAGAGTATATCTGTGCTTGGGAA 393
Qy      1956 TCTCACACAGAAACTCAGAGACCCCCCTGCTGAGCTAAGGAGTCTTATCTCTCAGG 2015
Db      394 TCTCACACAGAAACTCAGAGACCCCCCTGCTGAGCTAAGGAGTCTTATCTCTCAGG 453
Qy      2016 GGGGGTTTAAGTCCGTTTGCAATATATGTCGTTATTT 2054
Db      454 GGGGGTTTAAGTCCGTTTGCAATATATGTCGTTATTT 492
```

Search completed: February 8, 2005, 21:26:56
Job time : 6987.34 secs